

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 28, 2006, 22:50:52 ; Search time 254 Seconds
(without alignments)
8229.971 Million cell updates/sec

Title: US-10-626-126-6

Perfect score: 1176

Sequence: 1 atgtcggagtctaacggcac.....cccgatcagtatcttttga 1176

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*

1: /cgn2_6/ptodata/1/ina/1 COMB.seq.*

2: /cgn2_6/ptodata/1/ina/5 COMB.seq.*

3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*

4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*

5: /cgn2_6/ptodata/1/ina/H COMB.seq.*

6: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq.*

7: /cgn2_6/ptodata/1/ina/PE COMB.seq.*

8: /cgn2_6/ptodata/1/ina/RE COMB.seq.*

9: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	669	56.9	1173	3	US-09-414-010-1
2	669	56.9	1173	3	US-09-812-216-1
3	669	56.9	1173	3	US-09-875-076-13
4	158.4	13.5	1239	3	US-09-891-053-2
5	158.4	13.5	2700	3	US-09-891-053-5
6	138.4	11.8	1335	2	US-08-985-090-3
7	138.4	11.8	1335	3	US-09-165-543-3
8	138.4	11.8	1335	3	US-09-167-354-6
9	138.4	11.8	1335	3	US-09-642-855-6
10	138.4	11.8	1335	3	US-09-642-514-6
11	138.4	11.8	1335	3	US-09-642-852-6
12	138.4	11.8	2050	3	US-09-891-053-21
13	138.4	11.8	2665	3	US-09-949-016-5059
14	138.4	11.8	2689	2	US-08-985-090-1
15	138.4	11.8	2689	3	US-09-165-543-1
16	138.4	11.8	2689	3	US-09-167-354-5
17	138.4	11.8	2699	3	US-09-642-855-5
18	138.4	11.8	2699	3	US-09-642-514-5
19	138.4	11.8	2699	3	US-09-642-852-5
20	138	11.7	1338	3	US-09-165-543-6
21	138	11.7	1953	3	US-09-891-053-26
22	138	11.7	3244	3	US-09-165-543-4
23	89	7.6	1056	3	US-09-524-162-1
24	88.8	7.6	1086	2	US-08-985-090-6

RESULT 1
US-09-414-010-1
; Sequence 1, Application US/09414010
; Patent No. 6204017
; GENERAL INFORMATION:
; APPLICANT: Behan, Jjiang Xu
; APPLICANT: Hedrick, Joseph A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Monsma, Frederick J. Jr.
; APPLICANT: Morse, Kelley L.
; APPLICANT: Umland, Shelby P.
; APPLICANT: Wang, Suke
; TITLE OF INVENTION: Histamine receptor
; FILE REFERENCE: CN01069
; CURRENT APPLICATION NUMBER: US/09/414,010
; CURRENT FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-414-010-1

ALIGNMENTS

25	88.8	7.6	1086	3	US-09-165-543-33	Sequence 33, Appl
26	88.8	7.6	2218	2	US-08-985-090-4	Sequence 4, Appl
27	88.8	7.6	2218	3	US-09-165-543-31	Sequence 31, Appl
28	74	6.3	1401	3	US-09-826-509-514	Sequence 514, App
29	74	6.3	2210	3	US-09-016-434-1177	Sequence 1177, App
30	74	6.3	2210	3	US-10-166-199-1	Sequence 1, Appl
31	69.2	5.9	601	3	US-09-949-016-177027	Sequence 177027,
32	69.2	5.9	1893	3	US-09-891-053-13	Sequence 13, Appl
33	69.2	5.9	9293	3	US-09-949-016-16801	Sequence 16801, A
34	61.2	5.2	1386	3	US-09-016-434-1339	Sequence 1339, Ap
35	61.2	5.2	1422	3	US-09-826-509-512	Sequence 512, App
36	60.8	5.2	1581	2	US-08-313-553-8	Sequence 8, Appl
37	60.8	5.2	1581	3	US-08-767-993-8	Sequence 8, Appl
38	60.8	5.2	1956	2	US-08-313-553-6	Sequence 6, Appl
39	60.8	5.2	1956	3	US-08-767-993-6	Sequence 6, Appl
40	60	5.1	1233	3	US-09-721-870-176	Sequence 176, App
41	59.6	5.1	1599	3	US-09-826-509-520	Sequence 520, App
42	59.6	5.1	2261	3	US-09-016-434-1176	Sequence 1176, Ap
43	59	5.0	448	3	US-09-891-053-12	Sequence 12, Appl
44	58.4	5.0	1742	3	US-09-016-434-1411	Sequence 1411, Ap
45	56.8	4.8	4008	3	US-09-976-594-158	Sequence 158, App

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Db	61	TTTATGTCCTTAGTAGCTTTTGTATAATGCTAGGAATGCTTTGTCATTTAGCTTTT	120
Qy	121	GTACGACAGACAAACCTTAGACATCGAAGTAATATTTTTTCTTAATTTGGCTATTCT	180
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Qy 481 ACCAACACAGAGAGCTGGAGCTGGCTTTGTTACTGAGTGGTACATCTCGCCCATTTACA 540
Db 477 --TGAAGGTAGTGAATGGAACCTGGAATTTTTTCGGAATGGTACATCTTGCATCACA 534
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Db 535 TCATTTCTGGAATTCGTGATCCCACTCATCTTAGTCGCTTATTTCAACATGAATATTTAT 594
Qy 601 TGAAGCTGTGGAAGCTGGAGTCTCAGTAGTGGCCCTTAGCCACGCTGGAATTCATCGCT 660
Db 595 TGAAGCTGTGGAAGCTGATCATCTCAGTAGTGGCCCAAGCCATCTCTGACTGACTGCT 654
Qy 661 ACCTCTCCAGGGGCACTGGACACTCAGCAGAACTGGGTTGGCTTGTAGGCAAGTCTTT 720
Db 655 GTCTCTTCCAAACATCTGTGACACTCAATCAGAGGTAGACTATCTTCAAGGAGATCTTT 714
Qy 721 CCTGGAATTAAGGAACAGCGCGCATCCCTTCATTTCAGAAAGTCCACGAGGAAGAGAGT 780
Db 715 TCTGCATCGACAGAGTTCTGTCATCTTTCATTCAGAGAGACAGAGGAGAGAGTAGT 774
Qy 781 CTCTGCTGTCTTAAGGACTCATCAGAGCGGTAGTATCATGCGCTTCAAAGTGGGTTC 840
Db 775 CTCAATGTTTTCTTCAAGAACCAAGATGAATAGCAATACAATTCGTTCCAAAATGGGTTC 834
Qy 841 TCTCGCGATCAGAAAGCCAGTGTCTCACCAGAGAGGACCTGGAGCTTCTCAGAGGC 900
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Db 955 TATCTCTGTTCACAAATGTCCTTTCATTTTATTTCTCAGCAACAGGCTCCTAAATCAGTT 1014
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Db 1015 TGGTATAGAAATTCGATTTTGGCTTCAGTGGTTCATTTCTTGTCAATCTCTTTTGTAT 1074
Qy 1081 CCTTTGTGCCACAGAGCTTTCCAGAGGCTTTCTGGAAGATACTCTGTGTGACAAAGCAA 1140
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Qy 1141 CCAGCACTTTC---ACAGACCCAGTCAATTCATTCCTTGA 1176
Db 1135 CCTCTACCATCACAAACACAGTGGTGGTCAATTCCTTAA 1173
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RESULT 2

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US-09-812-216-1
; Sequence 1, Application US/09812216
; Patent No. 6613533
; GENERAL INFORMATION:
; APPLICANT: Behan, Jiang Xu
; APPLICANT: Hedrick, Joseph A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Monsma, Frederick J. Jr.
; APPLICANT: Morse, Kelley L.
; APPLICANT: Umland, Shelby P.
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; APPLICANT: Wang, Suke
; TITLE OF INVENTION: Histamine receptor
; FILE REFERENCE: CN01069
; CURRENT APPLICATION NUMBER: US/09/812,216
; CURRENT FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 09/414,010
; PRIOR FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-812-216-1
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Query Match 56.9%; Score 669; DB 3; Length 1173;

Best Local Similarity 74.2%; Pred. No. 6.3e-218;

Matches 875; Conservative 0; Mismatches 295; Indels 9; Gaps 2;

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Db 61 TTTATGTCCTTAGTAGCTTTTGTCTATAATGCTAGGAAATGCTTTGGTCAATTTTAGCTTT 120
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Db 655 GTCTCTTCCAAACATCTGTGACACTCAATCAGAGGTAGACTATCTTCAAGGAGATCTTT 714
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Db 1075 CCATTGTGTCAAGAGCTTTTCAAGAGGCTTTCTTGAATAATATTTGTATAAAAAAGCAA 1134
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Db 1135 CCTTACCATCACAACACAGTGGTCAAGTATCTTCTTAA 1173

RESULT 3

US-09-875-076-13
; Sequence 13, Application US/09875076
; Patent No. 6869776
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/09/875,076
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,127
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,131
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/141,448
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/156,653
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,633
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,555
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,634
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/157,280

; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,294
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,281
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,293
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,282
; PRIOR FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-875-076-13

Query Match 56.9%; Score 669; DB 3; Length 1173;
Best Local Similarity 74.2%; Pred. No. 6.3e-218;
Matches 875; Conservative 0; Mismatches 295; Indels 9; Gaps 2;

Qy 1 ATGTCGGAGTCTAAACGGCACTGACGCTCTGGCCACTGACTGCTCAAGTCCCTTGGCAATTT 60
Db 1 ATGCCAGATACTAATAGCACAAATCAATTTATCACTAAGCACTGCTGTTACTTTAGCATTT 60
Qy 61 TTAATGTCCTGCTTGTCTTTTGTCTATAACGATAGGCAATGCTGTGGTCAATTTAGCCTTT 120
Db 61 TTTATGTCTCTTAGTACTTTTGTCTATAAGTCTAGGAAATGCTTTGGTCAATTTAGCTTTT 120
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Qy 301 TCCGCTCTACAGTATGCTCTCAATTAGCTACGATCGATACCAAGTCAGTTCCTCAACGCTGTG 360
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Db 361 TCTTATAGAACTCAACATACACTGGGTCTTGAAGATTTGTTACTCTGATGGTGGCGTTTGG 420
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Db 421 GTGCTGGCTTCTTGTGTCATGAGCCCAATGATTTCTAGTTTTCAGAGTCTCTGGAAGGA--- 476
Qy 481 ACCAACACAGAGAGTGGCGAGCTGCTGTTGTTACTGAGTGGTACATCTCTCGCCATTACA 540
Db 477 --TGAAGGTAGTGAATGTGAACCTGGAATTTTTTCGGAATGGTACATCTCTGCGCATACA 534
Qy 541 GCATTTCTTGGAAATTTCTGCTGCTCTCTCTGCTGCTCTCTCTGCTGCTTACATGATTTAC 600
Db 535 TCATTTCTTGGAAATTTCTGCTGCTCTCTCTGCTGCTCTCTCTGCTGCTTACATGATTTAT 594
Qy 601 TGGAGCTGTGGAAGCGTGGAGTCTCAGTATGTCCTTAGCCACCGCTGATTCATCGCT 660
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Db 775 CTCATGTTTTCTTCAAGAACCAAGATGATAGCAATACAAATTGCTTCCAAAATGGGTTC 834
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RESULT 4

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US-09-891-053-2
; Sequence 2, Application US/09891053
; Patent No. 6750322
; GENERAL INFORMATION:
; APPLICANT: Itadani, Hiraku
; APPLICANT: Takimura, Tetsuo
; APPLICANT: Nakamura, Takao
; APPLICANT: Kobayashi, Masahiko
; APPLICANT: Tanaka, Ken-ichi
; APPLICANT: Hidaka, Yuseki
; APPLICANT: Ohta, Masataka
; TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)
; FILE OF INVENTION: BINDING PROTEIN-COUPLED RECEPTOR PROTEINS
; FILE REFERENCE: 06501-083001
; CURRENT APPLICATION NUMBER: US/09/891,053
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: PCT/JP99/07280
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: PCT/JP98/05967
; PRIOR FILING DATE: 1998-12-25
; PRIOR APPLICATION NUMBER: JP 11/145661
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1239
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1239)
US-09-891-053-2
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Query Match 13.5%; Score 158.4; DB 3; Length 1239;
Best Local Similarity 50.6%; Pred. No. 4.9e-43;
Matches 551; Conservative 0; Mismatches 516; Indels 23; Gaps 6;

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QY 51 CTTGGCATTTTAAATGCTTCCTGCTGCTTTTGTCTATAACGATAGGCAATGCTGTGTCAT 110
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Db 108 CTTGGCTGGCTCATGGCGCTGCTCATCTGTGGCCACAGTACTGGGCAACGCGTGTAT 167
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 111 TTTAGCCTTTGTAGCAGACAGAAACCTTAGACATCGAAGTAATTTTCTTAATTT 170
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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RESULT 5
US-09-891-053-5

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Db 168 GCTCGCCTTTCTGGGGGATTCGAGCCTTCGCAACCCAGAACAACTTCTTCTGCTCAACCT 227
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 171 GGTATTTCTGACTTCTTCTGSGGTGTCATCTCCATTCCTCTGTACATCCCTCACACGCT 230
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 228 CGCCATCTCCGACTTCTCTGSGGTGCTTCTGCAATCCCATTTGTAGTACCTTATGTGCT 287
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 231 GTTTAAAC---TGGAATTTTGGAAAGTGGAAATCTGCAATGTTTGGCTCATTTACTGACTATCT 287
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 288 GACCGGCGGTGGACCTTCGGCGGGGCTCTGCAAGCTGTGGCTGGTGGTAGACTACCT 347
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 288 TTTGTGCACAGCATTCGCTCTACAGTATTTCTCTCAATAGCTACGATCGATCGATACAGTCAGT 347
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 348 ACTGTGTGCTCTCTCGGCTTCAACATCTGTAATCATCAGTATGACCGGATTCCTGTGAGT 407
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QY 348 TTTCAAACGCTGTGCGTTATAGAGCACAGCACACTGSCATCTCTGAAAATTTGTTGCTCAAT 407
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 408 CACTCGAGCTGTCTCTACAGGGCCAGCAGGGGGACACGAGACGGGCGCTTTCGGGAAT 467
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 408 GGTGGCTGTTTGGATACTGGCTTTCTTGGTCAATGGCCCAATGATTTCTGGCTTTCGGAT-- 465
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 468 GGCATCTGTTGTTGGTGTGGCTTCTGCTGTATGGGCTGCGCATCTGAGTTGGGAGTA 527
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 466 ----TCTTGGAAAGAACAGACCAACACAGAGAGTGGAGCCTGGCTTTGTTACTGAGTG 521
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 528 CTTGTCTGGTGGCAGTTCCATCCCGAGGGCCACTGCTATGCTGAGTTCTTCTACAACTG 587
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 522 GTACATCTCGCCATTACAGCAATTTGGAATTTCTGCTCCCTGCTCTCTCTGTTGGTCTTA 581
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 588 GTACTTTCTCATCGGCTTCCACCTCGAGTCTTACGGCTTCTCAGGCCCTTCTCAGCGTTACCTT 647
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 582 TTTTCACTGTACAGATTTTACTCGGAGCTGTGGAAGGCTGGGAGTCTCAGTAGGTGCCCTAG 641
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 648 CTTTCAACCTCAGCATCTACTGTGAACATCAGAGGGCGCACCCGCTTCGGCTTGTAGTGGGG 707
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 642 CCAGCTGATTTATCGCTACTCTTTCAGGG- ----GCATGTGACACTCAACGAGAACTG 697
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 708 CCGTGAGGCTGGCCAGAAACCCCAACAGATGCCAGCCCTCGCCACCTCCAGCTCCCCC 767
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 698 GGTTCGCTTTAGGACAAAGTCTTCTCGGATTTAAAGAACCCAGCCGCTCCCTTCTTCTAG 757
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 768 CAGCTGCTGGGCTGCTGGCCAAAAGGGCATGGCAGGCCATGCGGTTTGCA CAGCTCTGG 827
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 758 AAAGTCCACGAGAAAGACAGTCTCTCTGGTGTCTTAAAGGACTCACATGAGCGGTAGTA 817
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 828 CAGCTCTCAAGGGGCACTGAGAGGCCACGCTCACTCAA--AAGGGCTCCAAGCCATCA 885
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 818 TCATCGCCTTCAAAGTGGGTTCTTCTGCGGATCAGAAAGCCAGTGTCTTCCAGAGAG 877
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 886 GCATCTTCAGCATCCCTGGAGAAAGCGCATGAAAGATGGTGTCCAGAGCATCACC-----C 940
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 878 AGCAGTGGAGCTTCTCAGAGGCGAGGAGCTAGCCAGTGCCTAGCTGTCTCTGAGTG 937
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 941 AGCGCTTCGGCTGTGCGGGGCAAGAGGTGGCCAAAGTGCCTGGCCATCATCTGTGAGCA 1000
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 938 CTTTTGCCATTTTGGGCTCCGTAATTGCTTTTCCAAATTTGTTCTTTTCAACTTATCGCA 997
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1001 TCTTTGGGCTGCTGGGGCGGTACACGCTCTCTAATGATCATCCGAGCTGCTTGCATG 1060
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 998 GAGGGAGCGCCCCAAATCGATTTGGTACAGCATAGCCTTTTGGCTACAGTGGTTCAAAT 1057
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1061 GCCGCTGCATCCCCGATT---ACTGGTACGAGACGCTCTTCTGTGGCTTCTGTGGGCACT 1117
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1058 CACTTATTAATCCCTTTCTATACCTTTTGTGCCACAGAGCTTTCCAGAGGCTTCTTGA 1117
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1118 CGCGCGTCAACCCGCTCTCTACCCACTGTGCCACTACAGCTTCCGAGAGCTTCAACCA 1177
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1118 AGATACTCTG 1127
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1178 AGCTCTCTG 1187
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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```
/
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617)227-7400
/ TELEFAX: (617)742-4214
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1335 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 1..1335
US-08-985-090-3

Query Match      11.8%; Score 138.4; DB 2; Length 1335;
Best Local Similarity 54.8%; Pred. No. 3.7e-36;
Matches 321; Conservative 0; Mismatches 256; Indels 9; Gaps 2;

QY 53 TGGCATTTTAAATGTCCTGCTGCTTTTGTCTATAACGATAGGCAATGCTGTGTCATTT 112
DB 110 TGGCCGGCTCATGGCGCTGCTCATCGTGGCCACGGTGTGGGCAACGGCTGTGTCATGC 169
QY 113 TAGCCTTTGTAGCAGACAGAAACCTTAGACATCGAAGTAATTAATTTTCTTAATTGG 172
DB 170 TCGCCTTCGTGGCGGACTCGAGCCTCGCACCCAGAACAACTTCTTCTGCTCAACCTCG 229
QY 173 CTATTTCTGACTTCTTCTGCTGGTGTCTATCTCCATCTCTGTATACCTCCACAGCTG- 231
DB 230 CCATCTCCGACTTCTCTGCTGGCGCTTCTGCATCCCACTGTATGACCTACGTCGTA 289
QY 232 --TTTAACTGGAATTTTGAAGTGAATCTGCAATGTTTGGCTCATTACTGACTATCTTT 289
DB 290 CAGGCCGCTGACCTTCGGCGGGGCTCTGCAAGCTGTGGCTGTAGTGGACTACCTGC 349
QY 290 TGTGCACAGATCCGCTTACAGTATTGTCTCTCAATTAGCTACGATCGATACCACTGAGTTT 349
DB 350 TGTGCACCTCTCTGCTCTTCAACATCGTGTCTCATCAGTACGACCGCTTCTGTCGTC 409
QY 350 CAAACGCTGTGGTTATAGACACAGCACACTGGCATCTCTGAAATTTGTTGCTCAATGG 409
DB 410 CCGAGCGGTCTCATACCGGGCCACAGCGGTGACACGGCGGGGAGTGGCGAAGATGC 469
QY 410 TGGCTGTTTGGATACCTGGCTTTCTTGGTCAATGGCCCAATGATTCTGGCTTCGGA---- 464
DB 470 TGTGTGTGGGTGTGCTGGCTTCTCTGTATCGGACCAAGCCATCTCTGAGCTGGAGTACC 529
QY 465 -TTCTTTGGAAGAACAGACACCAACAGAGAGTGGAGCTGGCTTTGTTACTGAGTGGT 523
DB 590 ACTTCTCATCAGGCTTCCACCTGGAGTCTTTTACGCCCTTCTTACGCCCTTCTCAGGCTCACCTTCT 649
QY 584 TCAGTGTACAGATTACTGCGAGCTGTGGAGCGTGGAGTCTCAG 629
DB 650 TTAACCTCAGCATCTACCTGAACATCCAGAGGCGCACCCGCCCTCCG 695

RESULT 7
US-09-165-543-3
; Sequence 3, Application US/09165543
; Patent No. 6093545
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl and Sandra Glucksmann
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
```

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/ COUNTRY: USA
/ ZIP: 02109
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/165,543
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/042,780
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Elizabeth A. Hanley
/ REGISTRATION NUMBER: 33,505
/ REFERENCE/DOCKET NUMBER: MNI-032CP
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617)227-7400
/ TELEFAX: (617)742-4214
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1335 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 1..1335
US-09-165-543-3

Query Match      11.8%; Score 138.4; DB 3; Length 1335;
Best Local Similarity 54.8%; Pred. No. 3.7e-36;
Matches 321; Conservative 0; Mismatches 256; Indels 9; Gaps 2;

QY 53 TGGCATTTTAAATGTCCTGCTGCTTTTGTCTATAACGATAGGCAATGCTGTGTCATTT 112
DB 110 TGGCCGGCTCATGGCGCTGCTCATCGTGGCCACGGTGTGGGCAACGGCTGTGTCATGC 169
QY 113 TAGCCTTTGTAGCAGACAGAAACCTTAGACATCGAAGTAATTAATTTTCTTAATTGG 172
DB 170 TCGCCTTCGTGGCGGACTCGAGCCTCGCACCCAGAACAACTTCTTCTGCTCAACCTCG 229
QY 173 CTATTTCTGACTTCTTCTGCTGGTGTCTATCTCCATCTCTGTATACCTCCACAGCTG- 231
DB 230 CCATCTCCGACTTCTCTGCTGGCGCTTCTGCATCCCACTGTATGACCTACGTCGTA 289
QY 232 --TTTAACTGGAATTTTGAAGTGAATCTGCAATGTTTGGCTCATTACTGACTATCTTT 289
DB 290 CAGGCCGCTGACCTTCGGCGGGGCTCTGCAAGCTGTGGCTGTAGTGGACTACCTGC 349
QY 290 TGTGCACAGATCCGCTTACAGTATTGTCTCTCAATTAGCTACGATCGATACCACTGAGTTT 349
DB 350 TGTGCACCTCTCTGCTCTTCAACATCGTGTCTCATCAGTACGACCGCTTCTGTCGTC 409
QY 350 CAAACGCTGTGGTTATAGACACAGCACACTGGCATCTCTGAAATTTGTTGCTCAATGG 409
DB 410 CCGAGCGGTCTCATACCGGGCCACAGCGGTGACACGGCGGGGAGTGGCGAAGATGC 469
QY 410 TGGCTGTTTGGATACCTGGCTTTCTTGGTCAATGGCCCAATGATTCTGGCTTCGGA---- 464
DB 470 TGTGTGTGGGTGTGCTGGCTTCTCTGTATCGGACCAAGCCATCTCTGAGCTGGAGTACC 529
QY 465 -TTCTTTGGAAGAACAGACACCAACAGAGAGTGGAGCTGGCTTTGTTACTGAGTGGT 523
DB 530 TGTCCGGGGGCGAGCTCCATCCCGAGGCGCACTGCTATGCGGAGTCTTCTTCAACACTGGT 589
QY 524 ACATCTCGGCATTAAGCAATTTTGGAAATTCCTGCTCCCTGCTCTCTTGGTGGTCTATT 583
DB 590 ACTTCTCATCAGGCTTCCACCTGGAGTCTTTTACGCCCTTCTTACGCCCTTCTCAGGCTCACCTTCT 649
QY 584 TCAGTGTACAGATTACTGCGAGCTGTGGAGCGTGGAGTCTCAG 629
DB 650 TTAACCTCAGCATCTACCTGAACATCCAGAGGCGCACCCGCCCTCCG 695
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Qy 584 TCAGGTACAGATTACTGAGCGCTGTGGAGCGTGGAGTCTCAG 629
Db 650 TTAACCTCAGCATCTACCTGAACATCCAGAGCGCGCACCCGCTCCG 695

RESULT 8

US-09-167-354-6
; Sequence 6, Application US/09167354A
; Patent No. 6136559
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; FILE REFERENCE: SUBTYPE
; CURRENT APPLICATION NUMBER: US/09/167,354A
; PRIOR FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDNA
US-09-167-354-6

Query Match 11.8%; Score 138.4; DB 3; Length 1335;
Best Local Similarity 54.8%; Pred. No. 3.7e-36;
Matches 321; Conservative 0; Mismatches 256; Indels 9; Gaps 2;
Qy 53 TGGCAATTTTAAATGTCCTGCTGCTTTTGGCTATACGATAGGAATGCTGTGTCATTT 112
Db 110 TGGCGCGCTCATGGCGCTGCTCATCGTGGCCAGGTGCTGGGCAAGCGCTGTCATGC 169
Qy 113 TAGCCTTTGTAGCAGACAGAAACCTTAGACATCGAAGTAATATTTTCTTAATTTGG 172
Db 170 TCGCCTTCGTGGCGCACTCGAGCCTCGGCACCCAGAACTTCTTCTGCTCAACCTCG 229
Qy 173 CTATTTCTGACTTCTTGGAGTGGAAATCTGCAATGTTTGGCTCATTAAGTACTATCTTT 289
Db 230 CCATCTCCGACTTCTCGTGGCGCTTCTGCAATGCCATGATACCCCTACGTCGTA 289
Qy 232 --TTTAACTGGAATTTTGGAGTGGAAATCTGCAATGTTTGGCTCATTAAGTACTATCTTT 289
Db 290 CAGGCGCTGGACCTTTCGGCGGGGCTCTGCAAGCTGTGGCTGGTAGTGGACTACCTGC 349
Qy 290 TGTGCAAGCATCGTCTACAGTATTGCTCTCATTAGCTAGCTACGATCGATACAGTCAAGTTT 349
Db 350 TGTGCACTCTCTGCTTCAACATCGTGTCTCATGAGCTACGACCGCTTCTGTGCGTCA 409
Qy 350 CAAACGCTGCGTTATAGACACAGCACACCTGGCATCTGGAATAATGTTGCTCAATGG 409
Db 410 CCGAGCGGTCTCATACCGGGCCACAGAGGTGACACGGCGGGGCGAGTGGCGGAGATGC 469
Qy 410 TGGCTGTTGGATCTGCTGCTTCTTGGTCAATGGCCAAATGATTTGGCTTCGGA----- 464
Db 470 TGTGTTGGTGTGCTGGCTTCTGCTGTACGACCGAGCCATCTTGGAGTGGAGTACC 529
Qy 465 -TTCTTTGGAGAACACAGACCAACAGAGAGGTGGAGCTGGCTTGTACTGAGTGT 523
Db 530 TGTCCGGGGGAGCTCCATCCCGAGGGCCACTGCTATGCCGAGTCTTCTTCAAACTGGT 589
Qy 524 ACATCTCGGCATTAAGCAATTTTGGAAATTTCTGCTCCCTGCTCTGCTGGTGTCTATT 583
Db 590 ACTTCTCATCAGCGCTTCCACCTGGAGTCTTTAGCGCTTCTTCTCAGGCTCACCTTCT 649
Qy 584 TCAGGTACAGATTACTGAGCGCTGTGGAGCGTGGAGTCTCAG 629
Db 650 TTAACCTCAGCATCTACCTGAACATCCAGAGCGCGCACCCGCTCCG 695

RESULT 10

RESULT 9
US-09-642-855-6
; Sequence 6, Application US/09642855
; Patent No. 6413743
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; FILE REFERENCE: SUBTYPE
; CURRENT APPLICATION NUMBER: US/09/642,855
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: 09/167,354
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDNA
US-09-642-855-6

Query Match 11.8%; Score 138.4; DB 3; Length 1335;
Best Local Similarity 54.8%; Pred. No. 3.7e-36;
Matches 321; Conservative 0; Mismatches 256; Indels 9; Gaps 2;
Qy 53 TGGCAATTTTAAATGTCCTGCTGCTTTTGGCTATACGATAGGAATGCTGTGTCATTT 112
Db 110 TGGCGCGCTCATGGCGCTGCTCATCGTGGCCAGGTGCTGGGCAAGCGCTGTCATGC 169
Qy 113 TAGCCTTTGTAGCAGACAGAAACCTTAGACATCGAAGTAATATTTTCTTAATTTGG 172
Db 170 TCGCCTTCGTGGCGCACTCGAGCCTCGGCACCCAGAACTTCTTCTGCTCAACCTCG 229
Qy 173 CTATTTCTGACTTCTTGGAGTGGAAATCTGCAATGTTTGGCTCATTAAGTACTATCTTT 289
Db 230 CCATCTCCGACTTCTCGTGGCGCTTCTGCAATGCCATGATACCCCTACGTCGTA 289
Qy 232 --TTTAACTGGAATTTTGGAGTGGAAATCTGCAATGTTTGGCTCATTAAGTACTATCTTT 289
Db 290 CAGGCGCTGGACCTTTCGGCGGGGCTCTGCAAGCTGTGGCTGGTAGTGGACTACCTGC 349
Qy 290 TGTGCAAGCATCGTCTACAGTATTGCTCTCATTAGCTAGCTACGATCGATACAGTCAAGTTT 349
Db 350 TGTGCACTCTCTGCTTCAACATCGTGTCTCATGAGCTACGACCGCTTCTGTGCGTCA 409
Qy 350 CAAACGCTGCGTTATAGACACAGCACACCTGGCATCTGGAATAATGTTGCTCAATGG 409
Db 410 CCGAGCGGTCTCATACCGGGCCACAGAGGTGACACGGCGGGGCGAGTGGCGGAGATGC 469
Qy 410 TGGCTGTTGGATCTGCTGCTTCTTGGTCAATGGCCAAATGATTTGGCTTCGGA----- 464
Db 470 TGTGTTGGTGTGCTGGCTTCTGCTGTACGACCGAGCCATCTTGGAGTGGAGTACC 529
Qy 465 -TTCTTTGGAGAACACAGACCAACAGAGAGGTGGAGCTGGCTTGTACTGAGTGT 523
Db 530 TGTCCGGGGGAGCTCCATCCCGAGGGCCACTGCTATGCCGAGTCTTCTTCAAACTGGT 589
Qy 524 ACATCTCGGCATTAAGCAATTTTGGAAATTTCTGCTCCCTGCTCTGCTGGTGTCTATT 583
Db 590 ACTTCTCATCAGCGCTTCCACCTGGAGTCTTTAGCGCTTCTTCTCAGGCTCACCTTCT 649
Qy 584 TCAGGTACAGATTACTGAGCGCTGTGGAGCGTGGAGTCTCAG 629
Db 650 TTAACCTCAGCATCTACCTGAACATCCAGAGCGCGCACCCGCTCCG 695

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US-09-642-514-6
; Sequence 6, Application US/09642514
; Patent No. 6437100
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Brlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; FILE REFERENCE: SUBTYPE
; CURRENT APPLICATION NUMBER: US/09/642,514
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 09/167,354
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:CDNA
; US-09-642-514-6

Query Match      11.8%; Score 138.4; DB 3; Length 1335;
Best Local Similarity 54.8%; Pred. No. 3.7e-36;
Matches 321; Conservative 0; Mismatches 256; Indels 9; Gaps 2;

Qy 53 TGGCATTTTAAATGTCCTGCTGCTTTTGTCTATAACGATAGGCAATGCTGTGGTCATTT 112
Db 110 TGGCCGGCTCATGGCGCTCTCATCTGGCCACGGTGTGGGCAACGGCTGGTCATGC 169
Qy 113 TAGCCTTTGTAGCAGACAGAAACCTTAGACATCGAAGTAATTTTTCITTAATTGG 172
Db 170 TCGCCTTCGTGGCGACTCGAGCTCCGCCACCCAGAACAACTTCTTCTGCTCAACTCG 229
Qy 173 CTATTTCTGACTTCTTCTGTTGGTGTCTCATCTCCATTCTCTGATACCTCCCTCACAGCTG- 231
Db 230 CCATCTCCGACTTCTCTGTCGGCGCTTCTGATCCCACTGTATGTACCTACGTCGTA 289
Qy 232 --TTTAACTGGAATTTTGGAACTGTGAATCTGCATGTTTGGCTCATTACTGACTATCTTT 289
Db 290 CAGGCGCTGGGACTTTCGGCCGGGGCTCTGCAAGCTGTGGCTGGTAGTGGACTACTGC 349
Qy 290 TGTGCACAGCATCCGCTTACAGTATTGTCTCTCATTTAGCTACGATCGATACCACTCAGTTT 349
Db 350 TGTGCACCTCTCTGCTTCAACATGCTCTCATCAGCTAGCAGCCGCTTCTCTGCGTCA 409
Qy 350 CAAACGCTGTGCGTTATAGACACAGCACACTGGGATCTCTGAAATTTGTTGCTCAATGG 409
Db 410 CCGAGCGGTCTCATACCGGGCCAGCAGGTTGACACCGCGGGCAGTGCAGGAATGC 469
Qy 410 TGGCTGTTTGGATACGTGGCTTCTTGGTCAATGGCCCAATGATTCGTGGCTTCGGA---- 464
Db 470 TGTGTGTGGGTGCTGGGCTTCTCTGTATCGGACAGCCATCTCTGAGCTGGAGTACC 529
Qy 465 -TTCTTGGAAAGACAGACACAAACACAGAGAGAGTGGAGCTGGCTTGTTCAGTGGT 523
Db 530 TGTCCGGGGCAGCTCCATCCCGAGGGCCACTGCTATGCGAGTCTTCTTCACACTGGT 589
Qy 524 ACATCTTCGCAATTAAGCAATTTTGGAAATTTCTGCTCTCTCTCTCTCTCTCTCTCTCT 583
Db 590 ACTTCTCATCAAGGCTTCACTCCCGAGGGCCACTGCTATGCGAGTCTTCTTCACACTGGT 589
Qy 584 TCAGTGTACAGATTTACTGGAGCTGTGGAAAGCTGGAGTCTCAG 629
Db 650 TTAACCTCAGCATCTACCTGAACATCCAGAGGGCCACCCGCTCCG 695
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RESULT 12
US-09-891-053-21
; Sequence 21, Application US/09891053
; Patent No. 6750322
; GENERAL INFORMATION:

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Patent No. 6855560
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Brlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; FILE REFERENCE: SUBTYPE
; CURRENT APPLICATION NUMBER: US/09/642,852
; CURRENT FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: 09/167,354
; PRIOR FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:CDNA
; US-09-642-852-6

Query Match      11.8%; Score 138.4; DB 3; Length 1335;
Best Local Similarity 54.8%; Pred. No. 3.7e-36;
Matches 321; Conservative 0; Mismatches 256; Indels 9; Gaps 2;

Qy 53 TGGCATTTTAAATGTCCTGCTGCTTTTGTCTATAACGATAGGCAATGCTGTGGTCATTT 112
Db 110 TGGCCGGCTCATGGCGCTCTCATCTGGCCACGGTGTGGGCAACGGCTGGTCATGC 169
Qy 113 TAGCCTTTGTAGCAGACAGAAACCTTAGACATCGAAGTAATTTTTCITTAATTGG 172
Db 170 TCGCCTTCGTGGCGACTCGAGCTCCGCCACCCAGAACAACTTCTTCTGCTCAACTCG 229
Qy 173 CTATTTCTGACTTCTTCTGTTGGTGTCTCATCTCCATTCTCTGATACCTCCCTCACAGCTG- 231
Db 230 CCATCTCCGACTTCTCTGTCGGCGCTTCTGATCCCACTGTATGTACCTACGTCGTA 289
Qy 232 --TTTAACTGGAATTTTGGAACTGTGAATCTGCATGTTTGGCTCATTACTGACTATCTTT 289
Db 290 CAGGCGCTGGGACTTTCGGCCGGGGCTCTGCAAGCTGTGGCTGGTAGTGGACTACTGC 349
Qy 290 TGTGCACAGCATCCGCTTACAGTATTGTCTCTCATTTAGCTACGATCGATACCACTCAGTTT 349
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Qy 350 CAAACGCTGTGCGTTATAGACACAGCACACTGGGATCTCTGAAATTTGTTGCTCAATGG 409
Db 410 CCGAGCGGTCTCATACCGGGCCAGCAGGTTGACACCGCGGGCAGTGCAGGAATGC 469
Qy 410 TGGCTGTTTGGATACGTGGCTTCTTGGTCAATGGCCCAATGATTCGTGGCTTCGGA---- 464
Db 470 TGTGTGTGGGTGCTGGGCTTCTCTGTATCGGACAGCCATCTCTGAGCTGGAGTACC 529
Qy 465 -TTCTTGGAAAGACAGACACAAACACAGAGAGAGTGGAGCTGGCTTGTTCAGTGGT 523
Db 530 TGTCCGGGGCAGCTCCATCCCGAGGGCCACTGCTATGCGAGTCTTCTTCACACTGGT 589
Qy 524 ACATCTTCGCAATTAAGCAATTTTGGAAATTTCTGCTCTCTCTCTCTCTCTCTCTCTCT 583
Db 590 ACTTCTCATCAAGGCTTCACTCCCGAGGGCCACTGCTATGCGAGTCTTCTTCACACTGGT 589
Qy 584 TCAGTGTACAGATTTACTGGAGCTGTGGAAAGCTGGAGTCTCAG 629
Db 650 TTAACCTCAGCATCTACCTGAACATCCAGAGGGCCACCCGCTCCG 695
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RESULT 11
US-09-642-852-6
; Sequence 6, Application US/09642852

APPLICANT: Itadani, Hiraku
APPLICANT: Takimura, Tetsuo
APPLICANT: Nakamura, Takao
APPLICANT: Kobayashi, Masahiko
APPLICANT: Tanaka, Ken-ichi
APPLICANT: Hidaka, Yusuke
APPLICANT: Ohta, Masataka
TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)
TITLE OF INVENTION: BINDING PROTEIN-COUPLED RECEPTOR PROTEINS
FILE REFERENCE: 06501-083001
CURRENT APPLICATION NUMBER: US/09/891.053
CURRENT FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: PCT/JP99/07280
PRIOR FILING DATE: 1999-12-24
PRIOR APPLICATION NUMBER: PCT/JP98/05967
PRIOR FILING DATE: 1998-12-25
PRIOR APPLICATION NUMBER: JP 11/145661
PRIOR FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 21
LENGTH: 2050
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CD8
LOCATION: (271)....(1629)
US-09-891-053-21

Query Match 11.8%; Score 138.4; DB 3; Length 2050;
Best Local Similarity 54.8%; Pred. No. 4.9e-36;
Matches 321; Conservative 0; Mismatches 256; Indels 9; Gaps 2;
QY 53 TGGCAATTTTAAAGTCCTGCTGCTTTTGGCTATACGATAGGCAATGCTGTGCTCATTT 112
DB 380 TGGCCGGCTCATGGCGCTGCTCATGCTGGCCACGGTGTGGCCACGCGTGGTCATGC 439
QY 113 TAGCCTTTGTAGCAGACAGAAACCTTAGACATCGAAGTAATATTTTCTTAATTGG 172
DB 440 TCGCCTTGTGGCGGACTCGAGCCTCCGCCACCCAGAACAACTTCTTCTGCTCAACCTG 499
QY 173 CTATTTCTGACTTCTTGTGGGTGCTCATCTCCATTCTCTGTATACATCCCTCACAGCTG- 231
DB 500 CCATCTCCGACTTCTCTGTGGCGCTTCTGATCCCACTGATGATACCTACCTGCTGA 559
QY 232 --TTTAACTGGAATTTTGGAGTGGAACTCTGCAATGTTTGGCTCATTTACTGACTATCTTT 289
DB 560 CAGCCGCTGGACCTTCGCGCGGGGCTCTGCAAGCTGTGGCTGTAGTGAACCTACCTGC 619
QY 290 TGTGCA CAGCATCCGCTTACAGTATTCTCTCATTTAGCTACGATCGATACAGTCACTTT 349
DB 620 TGTGCACTCTCTGCTTCAACATCTGCTCATCAGTACGACGCGCTTCTGTGCGTCA 679
QY 350 CAAACGCTGTGGTTATAGAGCAGACACATGCGATCTCGAAATTTGTTGCTCAATGG 409
DB 680 CCGAGCGGTCTCATACCGGGCCAGCAGGGTGACACGCGCGGGGAGTGGGAGATGC 739
QY 410 TGGCTGTTGGTACTCGCTTTCTTGGTCAATGAGCCCAATGATCTGGCTTCGGA----- 464
DB 740 TGTGGTGTGGGTGCTGGCTTCTGCTGTAGGACAGCCNCTTGAAGTGGAGTACC 799
QY 465 -TTCTTGGAGAGACAGACCAACACAGAGAGTGGAGCTGGCTTTGTTACTGAGTGGT 523
DB 800 TGTCCGGGGGAGCTCCATCCCGAGGGCCACTGCTATGCGGAGTCTTCTTACAACTGGT 859
QY 524 ACATCTCGGCATTTACAGCATTTTGGAAATCTTGGTCTCCCTGCTCCCTGCTGCTATT 583
DB 860 ACTTCTCATCAGGGCTTCACCCCTGGAGTCTTTTACGCCCTTCTCCTCAGGCTCACCTTCT 919
QY 584 TCAGTGTACAGATTTACTGGAGCTGTGGAAGCTGGGAGTCTCAG 629
DB 920 TTAACCTCAGCATCTACCTGAAACATCCAGAGGGCGACCCCGCTCCG 965

RESULT 13
US-09-949-016-5059
Sequence 5059, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949.016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5059
LENGTH: 2665
TYPE: DNA
ORGANISM: Human
US-09-949-016-5059

Query Match 11.8%; Score 138.4; DB 3; Length 2665;
Best Local Similarity 54.8%; Pred. No. 5.9e-36;
Matches 321; Conservative 0; Mismatches 256; Indels 9; Gaps 2;
QY 53 TGGCAATTTTAAAGTCCTGCTGCTTTTGGCTATACGATAGGCAATGCTGTGCTCATTT 112
DB 401 TGGCCGGCTCATGGCGCTGCTCATGCTGGCCACGGTGTGGCCACGCGTGGTCATGC 460
QY 113 TAGCCTTTGTAGCAGACAGAAACCTTAGACATCGAAGTAATATTTTCTTAATTGG 172
DB 461 TCGCCTTGTGGCGGACTCGAGCCTCCGCCACCCAGAACAACTTCTTCTGCTCAACCTG 520
QY 173 CTATTTCTGACTTCTTGTGGGTGCTCATCTCCATTCTCTGTATACATCCCTCACAGCTG- 231
DB 521 CCATCTCCGACTTCTCTGTGGCGCTTCTGCAATCCCACTGATGATACCTACCTGCTGA 580
QY 232 --TTTAACTGGAATTTTGGAGTGGAACTCTGCAATGTTTGGCTCATTTACTGACTATCTTT 289
DB 581 CAGCCGCTGGACCTTCGCGCGGGGCTCTGCAAGCTGTGGCTGTAGTGAACCTACCTGC 640
QY 290 TGTGCA CAGCATCCGCTTACAGTATTCTCTCATTTAGCTACGATCGATACAGTCACTTT 349
DB 641 TGTGCACTCTCTTGGCTTCAACATCTGCTCATCAGTACGACGCGCTTCTGTGCGTCA 700
QY 350 CAAACGCTGTGGTTATAGAGCAGACACATGCGATCTCGAAATTTGTTGCTCAAAATGG 409
DB 701 CCGAGCGGTCTCATACCGGGCCAGCAGGGTGACACGCGCGGGGAGTGGGAGATGC 760
QY 410 TGGCTGTTGGTACTGCTTTCTTGGTCAATGAGCCCAATGATCTGGCTTCGGA----- 464
DB 761 TGTGGTGTGGGTGCTGCTTCTGCTGTACGGAACAGCCNCTTGAAGTGGAGTACC 820
QY 465 -TTCTTGGAGAGACAGACCAACACAGAGAGTGGAGCTGGCTTTGTTACTGAGTGGT 523
DB 821 TGTCCGGGGGAGCTCCATCCCGAGGGCCACTGCTATGCGGAGTCTTCTTACAACTGGT 880
QY 524 ACATCTCGGCATTTACAGCATTTTGGAAATCTTGGTCTCCCTGCTCCCTGCTGCTATT 583
DB 881 ACTTCTCATCAGGGCTTCACCCCTGGAGTCTTTTACGCCCTTCTCCTCAGGCTCACCTTCT 940
QY 584 TCAGTGTACAGATTTACTGGAGCTGTGGAAGCTGGGAGTCTCAG 629
DB 941 TTAACCTCAGCATCTACCTGAAACATCCAGAGGGCGACCCCGCTCCG 986
RESULT 14
US-08-985-090-1

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GenCore version 5.1.7
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(without alignments)
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Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1176	100.0	1176	8	US-10-626-445-6
2	1176	100.0	1176	9	US-10-626-126-6
3	1176	100.0	1176	9	US-10-626-398-6
4	958.4	81.5	1176	8	US-10-626-445-5
5	958.4	81.5	1176	9	US-10-626-126-5
6	958.4	81.5	1176	9	US-10-626-398-5
7	669	56.9	1173	3	US-09-812-216-1
8	669	56.9	1173	3	US-09-910-411-1
9	669	56.9	1173	3	US-09-875-076-13
10	669	56.9	1173	3	US-09-876-252-13
11	669	56.9	1173	5	US-10-052-193-1
12	669	56.9	1173	6	US-10-290-078-26
13	669	56.9	1173	6	US-10-273-983-13
14	669	56.9	1173	6	US-10-354-769-1
15	669	56.9	1173	6	US-10-393-807-13
16	669	56.9	1173	6	US-10-417-820A-13
17	669	56.9	1173	7	US-10-349-253A-1
18	669	56.9	1173	7	US-10-723-955-13
19	669	56.9	1173	7	US-10-782-596-13
20	669	56.9	1173	7	US-10-737-619-1
21	669	56.9	1173	8	US-10-626-445-1
22	669	56.9	1173	9	US-10-616-088-1
23	669	56.9	1173	9	US-10-626-126-1

24	669	56.9	1173	9	US-10-626-398-1	Sequence 1, Appli
25	669	56.9	1173	9	US-10-723-955-13	Sequence 13, Appl
26	669	56.9	1265	6	US-10-290-078-25	Sequence 25, Appl
27	669	56.9	1265	3	US-10-488-421-5	Sequence 5, Appli
28	669	56.9	1266	3	US-09-891-138A-5	Sequence 5, Appli
29	669	56.9	1300	3	US-09-852-165-1	Sequence 1, Appli
30	669	56.9	1300	7	US-10-696-673-1	Sequence 1, Appli
31	669	56.9	3689	5	US-10-225-567A-628	Sequence 628, App
32	669	56.9	3689	8	US-10-684-206-19	Sequence 19, Appl
33	669	56.9	3689	9	US-10-756-149-32	Sequence 32, Appl
34	668	56.8	1170	9	US-10-488-421-7	Sequence 7, Appli
35	616.8	52.4	1170	8	US-10-626-445-7	Sequence 7, Appli
36	616.8	52.4	1170	9	US-10-626-126-7	Sequence 7, Appli
37	616.8	52.4	1170	9	US-10-626-398-7	Sequence 7, Appli
38	494.6	42.1	1166	9	US-10-488-421-3	Sequence 3, Appli
39	422.2	35.9	1103	9	US-10-488-421-1	Sequence 1, Appli
40	268.4	22.8	1326	7	US-10-398-036-19	Sequence 19, Appl
41	158.4	13.5	1239	8	US-09-891-053-2	Sequence 2, Appli
42	158.4	13.5	1239	8	US-10-759-463-2	Sequence 2, Appli
43	158.4	13.5	2700	8	US-09-891-053-5	Sequence 5, Appli
44	158.4	13.5	2700	8	US-10-759-463-5	Sequence 5, Appli
45	153	13.0	1311	9	US-10-495-679A-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-10-626-445-6
; Sequence 6, Application US/10626445
; Publication No. US20040248252A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0032
; CURRENT APPLICATION NUMBER: US/10/626,445
; CURRENT FILING DATE: 2003-07-23
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 6
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Rattus rattus
US-10-626-445-6

Query Match	100.0%	Score 1176;	DB 8;	Length 1176;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 1176;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	ATGTCGGAGTCTAACGGCACTGACGCTTGGCACTGACTGCTCAAGTCCCTCGCATTTT	60	
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Qy	61	TTAATGTCCTGCTTGTCTTTTGTATACGATGCAATGCTGTGTCATTTTAGCCCTTTT	120	
Db	61	TTAATGTCCTGCTTGTCTTTTGTATACGATGCAATGCTGTGTCATTTTAGCCCTTTT	120	
Qy	121	GTACGACAGAAACCTTAGACATCGAAGTAATTTTCTTAATTTGGCTATTTCCT	180	
Db	121	GTACGACAGAAACCTTAGACATCGAAGTAATTTTCTTAATTTGGCTATTTCCT	180	
Qy	181	GACTTCTTGGGTGTCATCTCAATTCCTCTGTACATCCCTCACAGCTGTTAACTGG	240	
Db	181	GACTTCTTGGGTGTCATCTCAATTCCTCTGTACATCCCTCACAGCTGTTAACTGG	240	
Qy	241	AATTTTGGAGTGAATCTGCATGCTTTTGGCTCAATTAATTTTGTGCACAGCA	300	
Db	241	AATTTTGGAGTGAATCTGCATGCTTTTGGCTCAATTAATTTTGTGCACAGCA	300	

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Db 361 CGTTATAGAGCACAGCACACTGGCATCTCTGAAATTTGTTCTCAAATGTTGGCTGTTGG 420
QY 421 ATACTGGCTTTCTTGTCATATGGCCCAATGATTTCTGGCTTCGGATTCCTTGGAAAGACAGC 480
Db 421 ATACTGGCTTTCTTGTCATATGGCCCAATGATTTCTGGCTTCGGATTCCTTGGAAAGACAGC 480
QY 481 ACCAAACACAGAGAGTCGAGCTGGCTTTGTTACTAGTGGTACATCTCTGCGCATTTACA 540
Db 481 ACCAAACACAGAGAGTCGAGCTGGCTTTGTTACTAGTGGTACATCTCTGCGCATTTACA 540
QY 541 GCATTTCTGGAAATTCCTGTCTCCCTGTCTCTCTGGTGTCTATTTCAAGTGTACAGATTTAC 600
Db 541 GCATTTCTGGAAATTCCTGTCTCCCTGTCTCTCTGGTGTCTATTTCAAGTGTACAGATTTAC 600
QY 601 TGGAGCTGTGGAAGCGTGGAGTCTCAGTAGTGGCTTACGACAGCTGGATTCATCGCT 660
Db 601 TGGAGCTGTGGAAGCGTGGAGTCTCAGTAGTGGCTTACGACAGCTGGATTCATCGCT 660
QY 661 ACCTCTTCCAGGGGCACTGGACACTCAGCAGAACTGGGTTGGCTTGTAGGACAAGTCTT 720
Db 661 ACCTCTTCCAGGGGCACTGGACACTCAGCAGAACTGGGTTGGCTTGTAGGACAAGTCTT 720
QY 721 CTTGGATTTAAAGGAAACAGCGCGCATCCCTTCAATTCAGAAAGTCCACGAGGAAAGACAGT 780
Db 721 CTTGGATTTAAAGGAAACAGCGCGCATCCCTTCAATTCAGAAAGTCCACGAGGAAAGACAGT 780
QY 781 CTCTGTGTCTTAAGGACTCAGTAGGAGTATCATGAGGAGTATCATCGCTTCAAAGTGGTTCC 840
Db 781 CTCTGTGTCTTAAGGACTCAGTAGGAGTATCATGAGGAGTATCATCGCTTCAAAGTGGTTCC 840
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Db 841 TTCTGCGATCAGAAAGCCAGTGTCTTACCAGAGAGGACAGCTGGAGCTTCTCAGAGGC 900
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QY 961 TATTGCTGTTCATTAATGTTCTTTCAAATTCGAGAGGAGGAGCGCCCAATCGATT 1020
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Db 1021 TGGTACAGCATAGCTTTTGGCTACAGTGGTTCAATTCATTAATTAATCCCTTTCTATAC 1080
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QY 1141 CCAGCACCTTTCAGAGCCCAAGTCAGTATCTTCTTGA 1176
Db 1141 CCAGCACCTTTCAGAGCCCAAGTCAGTATCTTCTTGA 1176
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RESULT 2
US-10-626-126-6
; Sequence 6, Application US/10626126
; Publication No. US20050074770A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0033
; CURRENT APPLICATION NUMBER: US/10/626,126
; CURRENT FILING DATE: 2003-07-23

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; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Rattus rattus
; US-10-626-126-6

Query Match 100.0%; Score 1176; DB 9; Length 1176;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTCGGAGTCTAAACGGCACTGACGCTTGGCCACTGACTGCTCAAGTCCCTTTGGCATTT 60
Db 1 ATGTCGGAGTCTAAACGGCACTGACGCTTGGCCACTGACTGCTCAAGTCCCTTTGGCATTT 60
QY 61 TTAATGTCCTGCTTGTCTTAAACGATAGGCAATGCTGTGCTCAATTTTGTAGCTTT 120
Db 61 TTAATGTCCTGCTTGTCTTAAACGATAGGCAATGCTGTGCTCAATTTTGTAGCTTT 120
QY 121 GTAGCAGACAGAAACCTTAGACATCGAAGTAAATTTTCTTAATTTGGCTATTTCT 180
Db 121 GTAGCAGACAGAAACCTTAGACATCGAAGTAAATTTTCTTAATTTGGCTATTTCT 180
QY 181 GACTTCTTGGGGTGTCTCTCCATTCCTGTGTAATCCCTCACAAGCTGTTTAACTGG 240
Db 181 GACTTCTTGGGGTGTCTCTCCATTCCTGTGTAATCCCTCACAAGCTGTTTAACTGG 240
QY 241 AATTTTGGAGTGGATCTGCAATGTTTGGCTCAATTCAGTATCTTTTGTGCACAGCA 300
Db 241 AATTTTGGAGTGGATCTGCAATGTTTGGCTCAATTCAGTATCTTTTGTGCACAGCA 300
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QY 421 ATACTGGCTTTCTTGTCATATGGCCCAATGATTTCTGGCTTCGGATTCCTTGGAAAGACAGC 480
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Qy     1141  CCAGCACCTTTCACAGAGCCCGAGTCAGTATCTTCTTGA 1176
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RESULT 3
US-10-626-398-6
; Sequence 6, Application US/10626398
; Publication No. US20050074841A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0034
; CURRENT APPLICATION NUMBER: US/10/626,398
; CURRENT FILING DATE: 2003-07-23
; PRIOR FILING DATE: 2003-07-23
; PRIOR FILING DATE: 2001-02-22
; PRIOR FILING DATE: 2001-02-22
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Rattus rattus
US-10-626-398-6
Query Match 100.0%; Score 1176; DB 9; Length 1176;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  ATGTCGGAGTCTAACCGCACTGAGCTCTTGCCACTGACTGCTCAAGTCCCTTTGGCATTT 60
Db      1  ATGTCGGAGTCTAACCGCACTGAGCTCTTGCCACTGACTGCTCAAGTCCCTTTGGCATTT 60
Qy     61  TTAATGTCCTGTGCTTTTGTCTATACGATAGGCAATGCTGTGTGCTATTTAGCCTTT 120
Db     61  TTAATGTCCTGTGCTTTTGTCTATACGATAGGCAATGCTGTGTGCTATTTAGCCTTT 120
Qy     121  GTAGCAGACAGAACCTTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTCT 180
Db     121  GTAGCAGACAGAACCTTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTCT 180
Qy     181  GACTTCTTCTGGGTGTCACTCCATTCCTCTGTACATCCCTCACAGCGTGTTAACCTGG 240
Db     181  GACTTCTTCTGGGTGTCACTCCATTCCTCTGTACATCCCTCACAGCGTGTTAACCTGG 240
Qy     241  AATTTTGGAAAGTGAATCTGCAATGTTTGGCTCATTAAGTATCTTTTGTGACAGCA 300
Db     241  AATTTTGGAAAGTGAATCTGCAATGTTTGGCTCATTAAGTATCTTTTGTGACAGCA 300
Qy     301  TCCGTCTACAGTATTGTCCTCATTAGCTAGCATCGATACAGTCAGTTCAAAGCGTGTG 360
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Db      301  TCCGTCTACAGTATTGTCCTCATTTAGCTACGATCCGATACCCAGTCAAGTTTCAAAGCGTGTG 360
Qy     361  CGTTATAGAGCACAGCACACTGGCATCTCGAAAATTTGTTGCTCAAAATGGTGGCTTTGG 420
Db     361  CGTTATAGAGCACAGCACACTGGCATCTCGAAAATTTGTTGCTCAAAATGGTGGCTTTGG 420
Qy     421  ATACTGGCTTTCTTTGGTCAATGATTCGATTCGCTTCGGATTCCTTGAAAGAACAGC 480
Db     421  ATACTGGCTTTCTTTGGTCAATGATTCGATTCGCTTCGGATTCCTTGAAAGAACAGC 480
Qy     481  ACCAACACAGAGAGAGTGCAGAGCCTGGCTTTGTTACTAGTGGTACATCTCTCGCCATPACA 540
Db     481  ACCAACACAGAGAGAGTGCAGAGCCTGGCTTTGTTACTAGTGGTACATCTCTCGCCATPACA 540
Qy     541  GCATTTCTGGAAATCTCTGCTCCCTGCTCTCTGCTGCTCTATTTCACTGTACAGATTAC 600
Db     541  GCATTTCTGGAAATCTCTGCTCCCTGCTCTCTGCTGCTCTATTTCACTGTACAGATTAC 600
Qy     601  TGGAGCTGTGGAAGCGTGGAGTCTCAGTAGTGCCTAGCCACGCTGGAATTCATCGCT 660
Db     601  TGGAGCTGTGGAAGCGTGGAGTCTCAGTAGTGCCTAGCCACGCTGGAATTCATCGCT 660
Qy     661  ACCTCTTCCAGGGGCACTGGACACTCAGCGCAGAACTGGGTTGGCTTGTAGGACAAAGTCTT 720
Db     661  ACCTCTTCCAGGGGCACTGGACACTCAGCGCAGAACTGGGTTGGCTTGTAGGACAAAGTCTT 720
Qy     721  CTTGGATTAAGGAACACAGCCGATCTCTTCAATTCAGAAAGTCCACGAGAGAAAGAGCAGT 780
Db     721  CTTGGATTAAGGAACACAGCCGATCTCTTCAATTCAGAAAGTCCACGAGAGAAAGAGCAGT 780
Qy     781  CTCCTGGTGTCTTAAGGACTCACATGAGCGGTAGTATCATCGCTTCAAAGTGGGTTC 840
Db     781  CTCCTGGTGTCTTAAGGACTCACATGAGCGGTAGTATCATCGCTTCAAAGTGGGTTC 840
Qy     841  TTCTGCCGATCAGAAAGCCAGTGTCTTCAACAGAGAGAGCACGTTGGAGCTTCTCAGAGGC 900
Db     841  TTCTGCCGATCAGAAAGCCAGTGTCTTCAACAGAGAGAGCACGTTGGAGCTTCTCAGAGGC 900
Qy     901  AGAAGCTAGCCAGGTGCTGCTGCTCTGAGTGTCTTTTGGCAATTTGCTGGGTCCG 960
Db     901  AGAAGCTAGCCAGGTGCTGCTGCTCTGAGTGTCTTTTGGCAATTTGCTGGGTCCG 960
Qy     961  TATTGCTGTTCACAAATGTTCTTCAACTATCGCAGAGGGGAGCGCCCAATCGATT 1020
Db     961  TATTGCTGTTCACAAATGTTCTTCAACTATCGCAGAGGGGAGCGCCCAATCGATT 1020
Qy    1021  TGGTACAGCAGTAGCTTTTGGCTACAGTGTGTTCAATTCATCTATTATCCCTTTCTATAC 1080
Db    1021  TGGTACAGCAGTAGCTTTTGGCTACAGTGTGTTCAATTCATCTATTATCCCTTTCTATAC 1080
Qy    1081  CCTTTGTGCCACAGAGCTTTTCCAGAGGCTTTCTGGAAGATACCTGTGTGACAAAGCAA 1140
Db    1081  CCTTTGTGCCACAGAGCTTTTCCAGAGGCTTTCTGGAAGATACCTGTGTGACAAAGCAA 1140
Qy    1141  CCAGCACCTTTCACAGAGCCCGAGTCAGTATCTTCTTGA 1176
Db    1141  CCAGCACCTTTCACAGAGCCCGAGTCAGTATCTTCTTGA 1176
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RESULT 4
US-10-626-445-5
; Sequence 5, Application US/10626445
; Publication No. US20040248252A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0032
; CURRENT APPLICATION NUMBER: US/10/626,445
; CURRENT FILING DATE: 2003-07-23
; PRIOR FILING DATE: 2003-07-23
; PRIOR FILING DATE: 2001-02-22
; PRIOR FILING DATE: 2001-02-22
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; PRIOR FILING DATE: 2000-05-31									
; NUMBER OF SEQ ID NOS: 27									
; SOFTWARE: PatentIn version 3.2									
; SEQ ID NO 5									
; LENGTH: 1176									
; TYPE: DNA									
; ORGANISM: Mus musculus									
US-10-626-445-5									
Query Match 81.5%; Score 958.4; DB 8; Length 1176;									
Best Local Similarity 88.4%; Pred. No. 6.4e-295;									
Matches 1040; Conservative 0; Mismatches 136; Indels 0; Gaps 0;									
QY	1	ATGTCGGAGTCTAAGCGCACTGACGCTCTTGCCACTGACTGCTCAAGTCCCTTGGCATTT	60						
Db	1	ATGTCGGAGTCTAAGCGCACTGACGCTCTTGCCACTGACTGCTCAAGTCCCTTGGCATTT	60						
QY	61	TTAATGTCCTGCTGCTTTGCTTAACGATAGGCAATGCTGTGCTCAATTTT	120						
Db	61	TTAATGTCCTGCTGCTTTGCTTAATGTTAGGCAATGCTGTGCTCAATTTT	120						
QY	121	GTAGCAGACAGAAACCTTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTTCT	180						
Db	121	GTGCTGACAGAAACCTTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTTCT	180						
QY	181	GACTTCTCTGTGGGTGTCATCTCCATTCCTCTGTACATCCCTCACAGCTGTTAACTG	240						
Db	181	GACTTCTCTGTGGGTGTCATCTCCATTCCTCTGTACATCCCTCACAGCTGTTAACTG	240						
QY	241	AAATTTGGAGTGGAAATCTGATGTTTGGCTCATTTACTGACTATCTTTTGGCAGCA	300						
Db	241	AAATTTGGAGTGGAAATCTGATGTTTGGCTCATTTACTGACTATCTTTTGGCAGCA	300						
QY	301	TCGCTCTACAGTATTTGCTCTCTTACATGATACAGTACAGTCAAGTCAAGCTGTG	360						
Db	301	TCGCTCTACAGTATTTGCTCTCTTACATGATACAGTACAGTCAAGTCAAGTGTG	360						
QY	361	CGTTATAGAGCAGCAGCAGCTGGCATCTCTGAAAAATTTGTTGCTCAAAATGGTGTG	420						
RESULT 5									
US-10-626-126-5									
; Sequence 5, Application US/10626126									
; Publication No. US20050074770A1									
; GENERAL INFORMATION:									
; APPLICANT: Lovenberg, Timothy									
; APPLICANT: Liu, Changlu									
; TITLE OF INVENTION: DNAB Encoding Mammalian Histamine Receptor Of The H4 Subtype									
; FILE REFERENCE: PRD-0033									
; CURRENT APPLICATION NUMBER: US/10/626,126									
; CURRENT FILING DATE: 2003-07-23									
; PRIOR APPLICATION NUMBER: 09/790,849									
; PRIOR FILING DATE: 2001-02-22									
; PRIOR APPLICATION NUMBER: 60/208,260									
; PRIOR FILING DATE: 2000-05-31									
; NUMBER OF SEQ ID NOS: 27									
; SOFTWARE: PatentIn version 3.2									
; SEQ ID NO 5									
; LENGTH: 1176									
; TYPE: DNA									
; ORGANISM: Mus musculus									
US-10-626-126-5									
Query Match 81.5%; Score 958.4; DB 9; Length 1176;									
Best Local Similarity 88.4%; Pred. No. 6.4e-295;									
Matches 1040; Conservative 0; Mismatches 136; Indels 0; Gaps 0;									
QY	1	ATGTCGGAGTCTAAGCGCACTGACGCTCTTGCCACTGACTGCTCAAGTCCCTTGGCATTT	60						
Db	1	ATGTCGGAGTCTAAGCGCACTGACGCTCTTGCCACTGACTGCTCAAGTCCCTTGGCATTT	60						
QY	61	TTAATGTCCTGCTGCTTTGCTTAACGATAGGCAATGCTGTGCTCAATTTT	120						
Db	61	TTAATGTCCTGCTGCTTTGCTTAATGTTAGGCAATGCTGTGCTCAATTTT	120						
QY	121	GTAGCAGACAGAAACCTTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTTCT	180						
Db	121	GTGCTGACAGAAACCTTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTTCT	180						
QY	181	GACTTCTCTGTGGGTGTCATCTCCATTCCTCTGTACATCCCTCACAGCTGTTAACTG	240						
Db	181	GACTTCTCTGTGGGTGTCATCTCCATTCCTCTGTACATCCCTCACAGCTGTTAACTG	240						
QY	241	AAATTTGGAGTGGAAATCTGATGTTTGGCTCATTTACTGACTATCTTTTGGCAGCA	300						
Db	241	AAATTTGGAGTGGAAATCTGATGTTTGGCTCATTTACTGACTATCTTTTGGCAGCA	300						
QY	301	TCGCTCTACAGTATTTGCTCTCTTACATGATACAGTACAGTCAAGTCAAGCTGTG	360						
Db	301	TCGCTCTACAGTATTTGCTCTCTTACATGATACAGTACAGTCAAGTCAAGTGTG	360						
QY	361	CGTTATAGAGCAGCAGCAGCTGGCATCTCTGAAAAATTTGTTGCTCAAAATGGTGTG	420						
Db	361	TCATTATAGGCTCAACACATGTCATCAAGATTTGTTGCTCAAAATGGTGTGTTG	420						
QY	421	ATACTGGCTTTCTTGCTCAATGCGCCCAATGATTTCTGGCTTCGGATTTCTTGGAGAAC	480						
Db	421	ATACTGGCTTTCTTGCTCAATGCGCCCAATGATTTCTGGCTTCAGATTTCTTGGAGAAC	480						
QY	481	ACCAACACAGAGAGTGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	540						
Db	481	ACCAACACAGAGAGTGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	540						
QY	541	GCAATTCCTGGAATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	600						
Db	541	ATGCTCTTGGAAATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	600						
QY	601	TGAGGCTCTGGAAGCTGGAGTCTCAGTAGTGGCTTACGCAAGCTGATTCATCGCT	660						
Db	601	TGAGGCTCTGGAAGCTGGAGTCTCAGTAGTGGCTTACGCAAGCTGATTCATCGCT	660						
QY	661	ACCTCTTCCAGGGGCACTGAGCACTCAACGAGAACTGGGTTGGCTTGTAGGCAAGTCTT	720						
Db	661	ACCTCTTCCAGTCTTTCAGGACCTTACACAGAGCTGGGTTGGCTTGTAGGCAAGTCTT	720						
QY	721	CCTGGATTAAGGAACCGCCATCCCTTCATTCAGAAAGTCCACGAGGAAGAGCAGT	780						
Db	721	CCTGGATTAAGGAATCAGCTGATCTCTGCTCCTCAGAAAGTCTCTGAAAGAAAGAGC	780						
QY	781	CTCCTGCTCTTAAAGGACTCACATGAGCGGTAGTATCATCGCTTCAAAGTGGGTTC	840						
Db	781	ATCTGCTGCTTAAAGGACTCACATGAGCAGGATATCATGCTTCAAAGTGGGTTC	840						
QY	841	TTCTGCGCATCAGAAAGCCAGTGTCTTACAGAGAGAGCAAGTGGAGCTTCTCAGAGG	900						
Db	841	TTCTGCGCATCGGAAAGTGTGAGGCTTTCGCAAGGGAGTACGAGAGAGCTTCTCAGAGG	900						


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Db 361 TCCTATAGGCTCAACACACTGGCATCATGAAGATTGTGCTCAATGGTGGCTGTTGG 420
Qy 421 ATACTGGCTTCTTGGTCAATGGCCCAATGATGTTCTGGCTCGGATTTCTTGGAGAACAGC 480
Db 421 ATACTGGCTTCTTGGTCAATGGCCCAATGATGTTCTGGCTCGGATTTCTTGGAGAACAGC 480
Qy 481 ACCAAACACAGAGGAGTGGAGCTGGCTTGTGTTACTGAGTGGTACATCTCGCCATTACA 540
Db 481 ACGAACAAAGGACTGTGAGCTGGCTTGTGTTACTGAGTGGTACATCTCGCCATTACA 540
Qy 541 GCATTTCTGGAAATTCCTGCTCCCTGCTCTCTGTTGGTGTCTATTTCACTGTACGATTTAC 600
Db 541 ATGCTCTTGGAAATTCCTGCTCCCTGCTCTCTGTTGGTGTCTATTTCACTGTACGATTTAC 600
Qy 601 TGGAGCTGTGGAAGCGTGGAGTCTCAGTAGTGGCTTACGACGCTGAGCCATCATCGCT 660
Db 601 TGGAGCTGTGGAAGCGTGGAGTCTCAGTAGTGGCTTACGACGCTGAGCCATCATCGCT 660
Qy 661 ACCTCTTCCAGGGCACTGGACACTCACGACGAGTGGTGGCTTGTAGGACAGTCTT 720
Db 661 ACCTCTTCCAGGGCACTGGACACTCACGACGAGTGGTGGCTTGTAGGACAGTCTT 720
Qy 721 CCTGGATTAAGGAACACAGCGCATCCCTTCAATTCAGAAAGTCCACGAGGAAGAGCAGT 780
Db 721 CCTGGATTAAGGAACACAGCGCATCCCTTCAATTCAGAAAGTCCACGAGGAAGAGCAGC 780
Qy 781 CTCTGTGTCTTAAAGGACTCACATGAGCGGTAGTATCATCGCTTCAAAGTGGGTTC 840
Db 781 ATCTGTGTCTTAAAGGACTCACATGAGCGGTAGTATCATCGCTTCAAAGTGGGTTC 840
Qy 841 TTCTGCCGATCAGAAAGCGGCTTCCAGAGGCTTCTGGAAGATACCTTGTGAGAACAA 1140
Db 841 TTCTGCCGATCAGAAAGCGGCTTCCAGAGGCTTCTGGAAGATACCTTGTGAGAACAA 1140
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Db 1021 TGGTACAGATAGGCTTTGGCTACAGTGGTCAATTCATCTATTAATCCCTTCTATAC 1080
Qy 1081 CCTTTGGCCACAGACGCTTCCAGAGGCTTCTGGAAGATACCTTGTGAGAACAA 1140
Db 1081 CCTTTGGCCACAGACGCTTCCAGAGGCTTCTGGAAGATACCTTGTGAGAACAA 1140
Qy 1141 CCAGGCTGTACAGAACCACTGATCTCTTTGA 1176
Db 1141 CCAGGCTGTACAGAACCACTGATCTCTTTGA 1176
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RESULT 6

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US-10-626-398-5
; Sequence 5, Application US/10626398
; Publication No. US20050074841A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0034
; CURRENT APPLICATION NUMBER: US/10/626,398
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
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; SEQ ID NO 5
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-626-398-5

Query Match      81.5%; Score 958.4; DB 9; Length 1176;
Best Local Similarity 88.4%; Pred. No. 6.4e-295;
Matches 1040; Conservative 0; Mismatches 136; Indels 0; Gaps 0;

Qy 1 ATGTGGAGTCTAAAGGCACTGACGCTTGGCCACTGACTGCTCAAGTCCCTTGGCAATTT 60
Db 1 ATGTGGAGTCTAAAGGCACTGACGCTTGGCCACTGACTGCTCAAGTCCCTTGGCAATTT 60
Qy 61 TTAATGTCCTGCTGCTTGTGCTATTAACGATAGGCAATGCTGTGGTCATTTTAGCCCTT 120
Db 61 TTAATGTCCTGCTGCTTGTGCTATTAACGATAGGCAATGCTGTGGTCATTTTAGCCCTT 120
Qy 121 GTAGCAGACAGAAACCTTAGACATCGAAATTAATTTTCTTAATTTGGCTATTTCT 180
Db 121 GTAGCAGACAGAAACCTTAGACATCGAAATTAATTTTCTTAATTTGGCTATTTCT 180
Qy 181 GACTTCTTGTGGGTGTCTCTCAATTCCTGTGTACATCCCTCACAGCTGTTTAACTGG 240
Db 181 GACTTCTTGTGGGTGTCTCTCAATTCCTGTGTACATCCCTCACAGCTGTTTAACTGG 240
Qy 241 AATTTTGGAGTGGAAATCTGCATGTTTGGCTCATTAAGTCTATCTTTTGGCAGCA 300
Db 241 AATTTTGGAGTGGAAATCTGCATGTTTGGCTCATTAAGTCTATCTTTTGGCAGCA 300
Qy 301 TCCGTCTACAGTATGTGCTCTTAGCTACGATCGATACCAAGTCAAGTCTGCTGTG 360
Db 301 TCCGTCTACAGTATGTGCTCTTAGCTACGATCGATACCAAGTCAAGTCTGCTGTG 360
Qy 361 CGTTATAGAGCAGACGACACTGGCATCTGGAATTTGTTCTCAAAATGGTGGCTGTTGG 420
Db 361 TCCTATAGGCTCAACACACTGGCATCATGAAGATTGTGCTCAAAATGGTGGCTGTTGG 420
Qy 421 ATACTGGCTTCTTGGTCAATGGCCCAATGATGTTCTGGCTCGGATTTCTTGGAGAACAGC 480
Db 421 ATACTGGCTTCTTGGTCAATGGCCCAATGATGTTCTGGCTCGGATTTCTTGGAGAACAGC 480
Qy 481 ACCAAACACAGAGGAGTGGAGCTGGCTTGTGTTACTGAGTGGTACATCTCGCCATTACA 540
Db 481 ACCAAACACAGAGGAGTGGAGCTGGCTTGTGTTACTGAGTGGTACATCTCGCCATTACA 540
Qy 541 GCATTTCTGGAAATTCCTGCTCCCTGCTCTCTGTTGGTGTCTATTTCACTGTACGATTTAC 600
Db 541 ATGCTCTTGGAAATTCCTGCTCCCTGCTCTCTGTTGGTGTCTATTTCACTGTACGATTTAC 600
Qy 601 TGGAGCTGTGGAAGCGTGGAGTCTCAGTAGTGGCTTACGACGCTGAGCCATCATCGCT 660
Db 601 TGGAGCTGTGGAAGCGTGGAGTCTCAGTAGTGGCTTACGACGCTGAGCCATCATCGCT 660
Qy 661 ACCTCTTCCAGGGCACTGGACACTCACGACGAGTGGTGGCTTGTAGGACAGTCTT 720
Db 661 ACCTCTTCCAGGGCACTGGACACTCACGACGAGTGGTGGCTTGTAGGACAGTCTT 720
Qy 721 CCTGGATTAAGGAACACAGCGCATCCCTTCAATTCAGAAAGTCCACGAGGAAGAGCAGT 780
Db 721 CCTGGATTAAGGAACACAGCGCATCCCTTCAATTCAGAAAGTCCACGAGGAAGAGCAGC 780
Qy 781 CTCTGTGTCTTAAAGGACTCACATGAGCGGTAGTATCATCGCTTCAAAGTGGGTTC 840
Db 781 ATCTGTGTCTTAAAGGACTCACATGAGCGGTAGTATCATCGCTTCAAAGTGGGTTC 840
Qy 841 TTCTGCCGATCAGAAAGCGGCTTCCAGAGGCTTCTGGAAGATACCTTGTGAGAACAA 900
Db 841 TTCTGCCGATCAGAAAGCGGCTTCCAGAGGCTTCTGGAAGATACCTTGTGAGAACAA 900
Qy 901 AGGAAGCTAGCCAGGCTGCTGCTGCTCTGCTGCTGCTTGTGCTGCTGCTGCTGCTGCTG 960
Db 901 AGGAAGCTAGCCAGGCTGCTGCTGCTCTGCTGCTGCTTGTGCTGCTGCTGCTGCTGCTG 960
Qy 961 AGGAAGCTAGCCAGGCTGCTGCTGCTCTGCTGCTGCTTGTGCTGCTGCTGCTGCTGCTG 960
Db 961 AGGAAGCTAGCCAGGCTGCTGCTGCTCTGCTGCTGCTTGTGCTGCTGCTGCTGCTGCTG 960
Qy 961 TATTGCTGTTCACAAATGTTCTTCAACTTATCGCAGAGGGGAGCGCCCAATCGATT 1020
Db 961 TACTGTCTGTTCACAAATGTTCTTCAACTTATCGCAGAGGGGAGCGCCCAATCGATT 1020
Qy 1021 TGGTACAGATAGGCTTTGGCTACAGTGGTCAATTCATCTATTAATCCCTTCTATAC 1080
Db 1021 TGGTACAGATAGGCTTTGGCTACAGTGGTCAATTCATCTATTAATCCCTTCTATAC 1080
Qy 1081 CCTTTGGCCACAGACGCTTCCAGAGGCTTCTGGAAGATACCTTGTGAGAACAA 1140
Db 1081 CCTTTGGCCACAGACGCTTCCAGAGGCTTCTGGAAGATACCTTGTGAGAACAA 1140
Qy 1141 CCAGGCTGTACAGAACCACTGATCTCTTTGA 1176
Db 1141 CCAGGCTGTACAGAACCACTGATCTCTTTGA 1176
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QY 961 TATTGCTGTTCACAAATGTTCTTTTCAACTTATCGCAGAGGGGAGCGGCCCAAAATCGATT 1020
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Db 961 TACTGTCTGTTCACAAATGTTCTTTCAACTTATCGCAGAGGGGAGCGGCCCAAAATCGGTG 1020
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QY 1021 TGGTACAGCATAGCCTTTTGGCTACAGTGGTTCAATTCATTATTAATCCCTTTCTATAC 1080
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Db 1021 TGGTACAGCATAGCCTTTTGGCTGCAATGTTCAATTCGTTTGTAAATCCCTTTCTGTAC 1080
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QY 1081 CCTTTGTGCCACAGAGCTTTCCAGAGGCTTTCTGGAAGATATCTCTGTGTGACAAAGCAA 1140
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Db 1081 CCTTTGTGTACAGGCTTTCCAGAGGCTTTCTGGAAGATATCTTTGTGTGACAAAGCAA 1140
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QY 1141 CCAGCAGCTTTCACAGAGCCAGTCAGTATCTTTCTTGA 1176
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Db 1141 CCAGCGCTGTTCACAGAACCAAGTCAGTATCTTTCTTGA 1176
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RESULT 7
US-09-812-216-1
; Sequence 1, Application US/09812216
; Patent No. US20020098539A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Jiang xu
; APPLICANT: Hedrick, Joseph A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Monsma, Frederick J. Jr.
; APPLICANT: Morse, Kelley L.
; APPLICANT: Umland, Shelby P.
; APPLICANT: Wang, Suke
; TITLE OF INVENTION: Histamine receptor
; FILE REFERENCE: CN01069
; CURRENT APPLICATION NUMBER: US/09/812,216
; CURRENT FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 09/414,010
; PRIOR FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-812-216-1

Query Match 56.9%; Score 669; DB 3; Length 1173;
Best Local Similarity 74.2%; Pred. No. 2.2e-202; Mismatches 295; Indels 9; Gaps 2;
Matches 875; Conservative 0;

QY 1 ATGTCGGAGTCTAACGGCACTGACGTCTTGCCACTGACTGCTCAAGTCCCTTGGCATTT 60
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Db 1 ATGCCAGATACTAATAGCAACAAATTTATCACTAAGCACTCGTGTACTTTAGCATTT 60
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 61 TTAATGTCCTGCTGTTGTTGTTGTTATTAACGATAGGCAATGCTGTGTGTCATTTAGCCTTT 120
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Db 61 TTTATGTCTCTTAGTAGCTTTTGTCTAATGCTAGGAAATGCTTTGGTCAATTTTAGCTTTT 120
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QY 121 GTAGCAGACAGAAACCTTACACATCGAAGTAATTTATTTTCTTAATTTGGCTATTCTTCT 180
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Db 121 GTGGTGACAAAACCTTAGACATCGAAGTAGTATTATTTTCTTAACCTTGGCCATCTCT 180
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 181 GACTTCTTCTGGGTGTGTCATCTCCATTCCTGTGTACATCCCTCACAGGCTGTTTAACTGG 240
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Db 181 GACTTCTTCTGGGTGTGATCTCCATTCCTTGTGTACATCCCTCACAGGCTGTTTGAATGG 240
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 241 AATTTTGAAGTGAATCTGATGTTTGTGCTCAATTAAGTCAATCTGACTATCTTTGTGCAAGCA 300
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 241 GAATTTGGAAGGAATCTGTGATTTTGGCTCACTACTGACTATCTGTTATGTATACAGCA 300
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 301 TCCGTCTACAGTATGTCCTCAATAGCTAGCATGATACAGTCAGTCAGTCAGTTTCAAAAGCTGTG 360
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 301 TCTGTATATAACATGTCCTCATCAGCTATGATGATGATGATGATGATGATGATGATGATGATG 360
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 361 CGTTATAGACACAGCACACTGGCATCTCTGAAAATTTGTTGCTCAAAATGTTGGTGTGTTGG 420
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

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Db 361 TCTTATAGAACTCAACATATCTGGGTCCTTGAAGATTGTTACTCTGATGTTGGCCGTTGG 420
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 421 ATACTGGCTTTCTTGTGTCATATGATTCGCTTCGGATTCCTGGATTCCTTGGGAAGAACAGC 480
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 421 GTGCTGGCTTCTTAGTGAATGGCCAAATGATTCAGATTCAGAGTCTTGGGAAGGA --- 476
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 481 ACCAACACAGAGAGAGTGCAGGCTGGCTTTGTTGTTACTAGTGTGTACATCTCGCCATTACA 540
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 477 --TGAAGGTAGTGAAATGTGAACCTGGATTTTTCGGAATGGTACATCTCTTGCATCACA 534
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 541 GCATTTCTTGGAAATTCCTGTCTCCCTGTCTCTTGGTGGTCTATTTTCAAGTGTACAGATTAC 600
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 535 TCAATTCCTTGGAAATTCGTGATTCCTCAGTCATCTTAGTCGCTTATTTCAACATGAATATTTAT 594
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 601 TGGAGCTGTGGAAGCGTGGAGTCTCAGTAGTGCCCTAGCCACACGCTGGATTCACTCGCT 660
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 595 TGGAGCTGTGGAAGCGGTGATCATCTCAGTAGTGCCAAAGCCATCTCTGGAGTACTGCT 654
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 661 ACCTCTTCCAGGGGCACTGGACACTCACGCAGAACTGGGTTGGCTTTGTAGGCAAACTCTT 720
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 655 GTCTCTTCCAAACATCTGTGGACACTCATTTCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 721 CTTGGATTAAGGAACAGCGGATCCCTTCAATTCAGAAAGTCCACAGAGGAAGAGCAGT 780
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 715 TCTGCATCGACAGAAAGTTCTCTGCATCTTTTCAATTCAGAGAGACAGAGGAGAAAGTAGT 774
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 781 CTCCTGCTGTCTTAAGGACTCACATGAGCGGTAGTATCATCGCCTTCAAAAGTGGGTTC 840
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 775 CTCATGTTTTCTCAAGAACCAAGATGAATGAATCAATTCATTTCCAAATGGGTTC 834
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 841 TTCTGCCGATCAGAAAGCCAGTGTCTTCCAGAGAGACACGTGGAGCTTCTCAGAGGC 900
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 835 TTCTCCCAATCAGATTCTGTAGCTCTTCAACAAAGGGAACATGTTGAACCTGTAGAGCC 894
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 901 AGAAGCTAGCCAGGTGCTAGTGTCTCTCCTGAGTGTCTTTTGCCATTTGCTGGGCTCCG 960
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 895 AGGAGATTAGCCAAAGTCACTGGCCATTTCTTAGGGGTTTTTGTCTGTTTGTGGGTCCA 954
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 961 TATTGCTGTTCACAAATGTTCTTTCACACTTATCGCAGAGGGGAGCGGCCCAAAATCGATT 1020
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 955 TATTCTGTGTACAAATGTCTTTTCAATTTATCTCTCAGCAACAGGTCTTAATCAGTT 1014
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1021 TGGTACAGCATAGCCTTTTGGCTACAGTGGTTTCAATTCATTTAATCCCTTTCTATAC 1080
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1015 TGGTATAGATTGCAATTTTGGCTTTCAGTGTTCATTTCTTGTCAATCTCTCTTTTGTAT 1074
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1081 CCTTTGTGCCACAGAGCTTTCAGAGGCTTTTCTGGAAGATATCTGTGTGACAAAGCAA 1140
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1075 CCATTTGTGTACAAAGCGCTTCAAAAGGCTTTCTTGAATAATATTTTGTATAAAAAAGCAA 1134
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1141 CCAGCACCTTC--ACAGACCCAGTCAGTATCTTCTTGA 1176
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1135 CCTTACCATCACACACAGTCGTCAGTATCTTCTTAA 1173
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 8
US-09-910-411-1
; Sequence 1, Application US/09910411
; Patent No. US20020137054A1
; GENERAL INFORMATION:
; APPLICANT: Bergsma, Derk
; APPLICANT: Fitzgerald, Laura
; APPLICANT: Li, Xiatong
; APPLICANT: Michalovich, David
; APPLICANT: Zhu, Yuan
; FILE REFERENCE: AXOR35, A G-Protein Coupled Receptor
; FILE REFERENCE: GP70655-2C1
; CURRENT APPLICATION NUMBER: US/09/910,411
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 09/693,761
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/497,790
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; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/431,898
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-910-411-1

Query Match          56.9%; Score 669; DB 3; Length 1173;
Best Local Similarity 74.2%; Pred. No. 2.2e-202; Mismatches 295; Indels 9; Gaps 2;
Matches 875; Conservative 0;

Qy 1 ATGTCGGAGTCTAAACGCACTGACGCTCTGCACTGCTGCTCAAGTCCCTTTGGCAATTT 60
Db 1 ATGCCAGATCTAATAGCAACAATCAATTTATCATCAAGCACTGCTGTTAGCAATTT 60

Qy 61 TTAATGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Db 61 TTAATGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120

Qy 121 GTAGCAGACAGAAACCTTAGACATCGAAGTAATTTTCTTAATTTGGCTATTTCT 180
Db 121 GTGTGGACAAAACCTTAGACATCGAAGTAGTATTTTCTTAATTTGGCTATTTCT 180

Qy 181 GACTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Db 181 GACTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240

Qy 241 AATTTGGAAGTGGAATCTGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
Db 241 GAATTTGGAAGGAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300

Qy 301 TCCGCTACAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
Db 301 TCTGTATATACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360

Qy 361 CGTTATAGACACAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
Db 361 TCTTATAGAACTCAACATCTGGGCTCTGAGATTTGTTACTCTGATGGTGGCGCTTGG 420

Qy 421 ATACTGCTTCTTGTGCTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
Db 421 GTGCTGCTTCTTGTGCTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 476

Qy 481 ACCAACACAGAGGAGTGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
Db 477 --TGAAGGTAGTGAATGTGAACCTGGATTTTTCGGAATGGTACATCCTTGGCCATCACA 534

Qy 541 GCATTCCTGGAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
Db 535 TCAATCTTGGAAATTCGATGATCCAGTCAATCTTGTGCTGCTTATTTCAACATGATTTAT 594

Qy 601 TGGAGCTCTGGAAGCTGGAGTCTCAGTAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
Db 595 TGGAGCTCTGGAAGCTGGATCATCTCAGTAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 654

Qy 661 ACCTTCTGAGGGCACTGACACATCAGCAGAACTGGTGGTGGTGGTGGTGGTGGTGGTGGT 720
Db 655 GTCTCTTCCAACTCTGTGACACTCAATTCAGAGGTAGACTATCTTCAAGGAGATCTCTTT 714

Qy 721 CCTGGAATTAAGGAACCAAGCGCATCTTCAATTCAGAAAGTCCACGAGGAAGAGAGAGT 780
Db 715 TCTGCATCGACAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 774

Qy 781 CTCTGCTGCTCTTAAGGACTCAATGAGCGGTAGTATCATGCTGCTTCAAGTGGGTTC 840
Db 775 CTCAATGTTTTCTCAAGAACCAAGATGAATAGCAATACAAATTTGCTTCAAAATGGGTTC 834

Qy 841 TTCTGCCGATCAGAAACCCAGTCTTCAACAGAGAGAGCAGTGGAGCTTCTCAGAGGC 900
Db 841 TTCTGCCGATCAGAAACCCAGTCTTCAACAGAGAGAGCAGTGGAGCTTCTCAGAGGC 900
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RESULT 9

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US-09-875-076-13
; Sequence 13, Application US/09875076
; Publication No. US20030017528A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huang T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCES: AREN0050
; CURRENT APPLICATION NUMBER: US/09/875,076
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,127
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,131
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/141,448
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/156,653
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,633
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,555
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,634
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/157,280
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,294
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,281
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; PRIOR FILING DATE: 1999-10-01
 ; PRIOR APPLICATION NUMBER: 60/157,293
 ; PRIOR FILING DATE: 1999-10-01
 ; PRIOR APPLICATION NUMBER: 60/157,282
 ; PRIOR FILING DATE: 1999-10-01
 ; NUMBER OF SEQ ID NOS: 74
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 13
 ; LENGTH: 1173
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-875-076-13

Query Match 56.9%; Score 669; DB 3; Length 1173;
 Best Local Similarity 74.2%; Pred. No. 2.2e-202;
 Matches 875; Conservative 0; Mismatches 295; Indels 9; Gaps 2;

QY	1	ATGTCGGAGCTTAACGGCACTGACGCTCTGCGCACTGCTCAAGTCCCTTCGGCATTT	60
DB	1	ATGCCAGATACTAATAGCAACAATTAATTAATCACTAAGCACTCGGTGTACTTTAGCATTT	60
QY	61	TTAATGTCCTGCTGCTCTTTGCTATAAGATAGGCAATGCTGTGGTCAATTTAGCCCTTT	120
DB	61	TTTAATGCTTAGTAGCTTTTGCTATAATGCTAGGAATGCTTTGGTCAATTTAGCTTTT	120
QY	121	GTAGCAGACAGAAACCTTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTCT	180
DB	121	GTGGTGGACAAAAACCTTAGACATCGAAGTAGTATTTTCTTAATTTGGCCATCTCT	180
QY	181	GACTTCTTGTGGGTGTATCTCCATCTCTCTGTATCATCCCTCACACGCTGTTAACTGG	240
DB	181	GACTTCTTGTGGGTGTATCTCCATCTCTCTGTATCATCCCTCACACGCTGTTGGAATGG	240
QY	241	AATTTTGGAGTGGAAATCGCATGTTTGGCTCATTTACTGACTATCTTTTGTGCACAGCA	300
DB	241	GAATTTGGAAAGAAATCTGTGTAATTTTGGCTCATCTACTGACTATCTTTATGTACAGCA	300
QY	301	TCCGCTCTACAGTATTGCTCTCAATAGCTACGATCGATACCACTCAGTCTTCAAAAGCTGTG	360
DB	301	TCGTGATATAACATTGCTCTCATCAGCTATGATCGATACCTGTCACTCTCAATGCTGTG	360
QY	361	CGTTATAGACAGACAGACACTGGCAATCTCGAAATATGTTGCTCAAAAGTGGCTGTTTGG	420
DB	361	TCATTATAGAACTCAACATACTGGGGTCTTGAAGATGTTTACTCTGATGGTGGCGGTTGG	420
QY	421	ATACTGGCTTCTTGTGCTCAATGGCCCAATGATTTCTGGCTTCGGATCTTGTGAAGACAGC	480
DB	421	GTCTGGCTTCTTAGTGAATGGGCCAATGATTTCTAGTATTAGAGTCTTGAAGA----	476
QY	481	ACCAACACAGAGAGTGGAGGCTGTGCTTTGTTTACTGAGTGGTATCATCTCGCCATTACA	540
DB	477	--TGAAGTAGTGAATGTGAACTCTGGAATTTTTCGGAAATGGTATCTCTGGCCATACA	534
QY	541	GCAATCTTGAATTCCTGCTCCCTGTCTCTCTGGTGGTCTATTTTCAGTGTACAGATTAC	600
DB	535	TCATTCTTGAATTCGTGATCCAGTCACTTTAGTCGCTTATTTTCAACATGAATATTAT	594
QY	601	TGAGGCTGTGGAGGCTGGAGTCTCAGTAGGTGCCCTAGCCAGCTGGATTATCGCT	660
DB	595	TGGAGGCTGTGGAAGCGGTGATCATCTCAGTAGGTGCCAAAGCCATCTCTGGACTGCT	654
QY	661	ACCTCTTCCAGGGGCACTGGACACTCACGCAACTGGGTTGGCTTTGTAGCAAGTCTTT	720
DB	655	GTCTCTTCCAACTCTGTGGAACTCATTTTCAGAGGTAGACTATCTTCAAGAGATCTCTT	714
QY	721	CCTGGATTAAAGAACCCAGCCGCTCCCTTCAATTCAGAAAGTCCACGAGGAAAGAGCAGT	780
DB	715	TCTGCATCGACAGAAAGTCTCTGCATCTTTTCAATTCAGAGACAGAGAGAGAGTAGT	774
QY	781	CTCCTGGTCTCTTAAGGACTCACATGAGCGGTAGTATCATCGCCCTTCAAAGTGGGTCC	840
DB	775	CTCATGTTTTCTTCAAGAACCCAGAGATGAATAGCAATACAATTTGCTTCCAAAATGGGTCC	834

RESULT 10
 US-09-876-252-13
 ; Sequence 13, Application US/09876252
 ; Publication No. US20030018182A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Behan, Dominic P.
 ; APPLICANT: Lehmann-Bruinsma, Karin
 ; APPLICANT: Chalmers, Derek T.
 ; APPLICANT: Lowitz, Kevin P.
 ; APPLICANT: Lin, I-Lin
 ; APPLICANT: Dang, Huong T.
 ; APPLICANT: Chen, Ruoping
 ; APPLICANT: Liaw, Chen W.
 ; TITLE OF INVENTION: Non-Endogenous Constitutively Activated Human G Protein Co
 ; FILE REFERENCE: AREN-0054
 ; CURRENT APPLICATION NUMBER: US/09/876,252
 ; CURRENT FILING DATE: 2001-06-07
 ; PRIOR APPLICATION NUMBER: 09/416,760
 ; PRIOR FILING DATE: 1999-10-12
 ; PRIOR APPLICATION NUMBER: 09/170,496
 ; PRIOR FILING DATE: 1998-10-13
 ; PRIOR APPLICATION NUMBER: 60/110,060
 ; PRIOR FILING DATE: 1998-11-27
 ; PRIOR APPLICATION NUMBER: 60/120,416
 ; PRIOR FILING DATE: 1999-02-16
 ; PRIOR APPLICATION NUMBER: 60/121,852
 ; PRIOR FILING DATE: 1999-02-26
 ; PRIOR APPLICATION NUMBER: 60/109,213
 ; PRIOR FILING DATE: 1998-11-20
 ; PRIOR APPLICATION NUMBER: 60/123,944
 ; PRIOR FILING DATE: 1999-03-12
 ; PRIOR APPLICATION NUMBER: 60/123,945
 ; PRIOR FILING DATE: 1999-03-12
 ; PRIOR APPLICATION NUMBER: 60/123,948
 ; PRIOR FILING DATE: 1999-03-12
 ; PRIOR APPLICATION NUMBER: 60/123,951
 ; PRIOR FILING DATE: 1999-03-12
 ; PRIOR APPLICATION NUMBER: 60/123,946
 ; PRIOR FILING DATE: 1999-03-12
 ; PRIOR APPLICATION NUMBER: 60/123,949
 ; PRIOR FILING DATE: 1999-03-12
 ; PRIOR APPLICATION NUMBER: 60/152,524
 ; PRIOR FILING DATE: 1999-09-03
 ; PRIOR APPLICATION NUMBER: 60/151,114
 ; PRIOR FILING DATE: 1999-08-27
 ; PRIOR APPLICATION NUMBER: 60/108,029
 ; PRIOR FILING DATE: 1998-11-12
 ; PRIOR APPLICATION NUMBER: 60/136,436

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; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,127
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,131
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/141,448
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/156,555
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,634
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,653
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/157,280
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,294
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,281
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,282
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/156,633
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-876-252-13

Query Match      56.9%; Score 669; DB 3; Length 1173;
Best Local Similarity 74.2%; Pred. No. 2.2e-202;
Matches 875; Conservative 0; Mismatches 295; Indels 9; Gaps 2;

QY      1  ATGTGGAGTCTACGGCACTGCTTGGCCACTGACTGCTCAAGTCCCTTGGCAATTT 60
DB      1  ATGCCAGATACTAATAGACAAATCAATTTATCACTAAGCACTCGTGTACTTTAGCAATTT 60
QY     61  TTAATGTCCTGCTGCTTTTGTCTATACGATAGGCAATGCTGTGGTCAATTTTAGCCTTT 120
DB     61  TTTATGTCCTTAGTAGCTTTTGTCTATATGCTAGGAATGCTTTGGTCAATTTTAGCTTTT 120
QY    121  GTAGCAGACAGAAACCTTAGACATCGAAGTAATTTTCTTAATTTGGCTATTTCCT 180
DB    121  GTGGTGACAAAAACCTTAGACATCGAAGTAGTTATTTTCTTAACCTTGGCCATCTCT 180
QY    181  GACTTCTTCTGGGTGTCATCTCCATTCCTCTGTACATCCCTCACAGCTGTTTAAGTG 240
DB    181  GACTTCTTCTGGGTGTCATCTCCATTCCTCTGTACATCCCTCACAGCTGTTTGAATG 240
QY    241  AATTTTGAAGTGAATCTGCATGCTTTTGGCTCAATTAAGTCACTATCTTTTGTGCACAGCA 300
DB    241  GATTTTGAAGAAGAAATCTGTGTATTTTGGCTCACTACTGACTATCTGTTATGTACAGCA 300
QY    301  TCGGTCTACAGTATGTCCTCATTPAGCTACGATCGATPACAGTCAAGTTCAAAACGCTGTG 360
DB    301  TCTGTATATAACATTTGCTCTCATCGCTATGATCGATACCTGTCAAGTCTCAATGCTGTG 360
QY    361  CGTTATAGACACAGCACTGGCATCTGAAATTTGCTGCTCAATGGTGGCTGTTTGG 420
DB    361  TCTTATAGAACTCAACATACCTGGGCTCTTGAAGATTTGTTACTCTGATGGTGGCGGTTGG 420
QY    421  ATACTGCTTTCTTGGTCAATGGCCCAATGATTCCTGGCTTGGGATTCCTGGAAGAACAGC 480
DB    421  GTGCTGGCCCTTCTTAGTGAATGGGCCAATGATTCCTAGATTTTCAAGAGTCTTGAAGGA---- 476

481  ACCAACACAGAGGAGTGGAGCGCTGCTTTGTACTGAGTGGTACATCCTCGCCATTACA 540
477  --TGAAGGTAGTGAATGTGAACCTGGATTTTTTTTGGAAATGGTATACCTTTGCCATTACA 534
541  GCATTTCTTGGAAATTCCTGCTCCCTGCTCTCTCTTGGTGTCTATTTTCAGTGTACAGATTTAC 600
535  TCATTTCTTGGAAATTCGTGATCCCAATCATCTTAGTCTGCTTATTTTCAACATGAATATTAT 594
601  TGGAGCCTGTGGAAGCGTGGAGTCTCAGTAGTGGCCCTTAGCCACGCTGGAATTCATCGCT 660
595  TGGAGCCTGTGGAAGCGTGTATCATCTCAGTAGTGGCCCAAGCCATCTCTGGACTGACTGCT 654
661  ACCTCTTCCAGGGGCACTGGACACTCAGCAGAACTGGCTTGGCTTGTAGGACAAGTCTT 720
655  GTCTCTTCCAAATCTCTGGACACTCATTCAGAGGTAGACTATCTTCAAGAGATCTCTT 714
721  CCTGGATTAAAGGAACCCAGCGCATCCCTTCATTCAGAAAGTCCACGAGGAAGAGCAGT 780
715  TCTGATCGACAGAGTTCCTGCTATCTTTCATTCAGAGAGACAGAGAGAGAGTAGT 774
781  CTCCTGTGTCTTAAAGGACTCAGATGAGGGGTAGTATCATCTGCTTCAAAAGTGGGTTC 840
775  CTCATGTTTCTCAAGAACCAAGATGAATAGCAATACAAATTTGCTTCCAAAATGGGTTC 834
841  TTCTGCGGATCAGAAAGCCAGTGTCTCACAGAGAGACAGCTGGAGCTTCTCAGAGGC 900
835  TTCTCCCAATCAGATTCGTAGCTTTCACAAAGGGAACATGTTGAACCTGCTTAGAGCC 894
901  AGGAAGCTAGCAGGTGCTGCTGCTCTGAGTGTCTTTGCAATTTTGGCAATTTGCTGGGCTCG 960
895  AGGAGATTAGCAAGTCACTGGCCATCTCTTAGGGGTTTTTGTGTTTGTGCTGGGCTCCA 954
961  TATTGCTGTTCACAAATGTTCTTTTCAACTTATGCGAGAGGGAGCGCCCAAAATCGATT 1020
955  TATTCTCTGTTCAAAATGTTCTTTTCACTTTTATTTCTCAGCAACAGGCTCTTAATCAGTT 1014
1021  TGGTACAGCATAGCCTTTTGGCTACAGTGTCTCAATTCATCTATTATTCCTTTCTATAC 1080
1015  TGGTATAGAAATTCATTTTGGCTTTCAGTGGTTCATTTCTTGTCAATCTCTTTTGTAT 1074
1081  CCTTTGGCCACAGAGCTTTCCAGAGGCTTTCTGGAAGATACCTCTGTGTGACAAAGCAA 1140
1075  CAATTTGTCTCAGAGCGCTTTCAAAAGGCTTTCTGAAATATTTTGTATATAAAGAAAGCAA 1134
1141  CCAGCACCTTTC---ACAGACCCAGTCAATATCTTCTTGA 1176
1135  CCTTACCATCACACACAGCTCGTCAATCTTCTTAA 1173

RESULT 11
US-10-052-193-1
; Sequence 1, Application US/10052193
; Publication No. US20020132755A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer, Inc.
; TITLE OF INVENTION: HISTAMINE RECEPTOR ANTAGONISTS
; FILE REFERENCE: PC10963A
; CURRENT APPLICATION NUMBER: US/10/052,193
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 0101223.6
; PRIOR FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-052-193-1

Query Match      56.9%; Score 669; DB 5; Length 1173;
Best Local Similarity 74.2%; Pred. No. 2.2e-202;
Matches 875; Conservative 0; Mismatches 295; Indels 9; Gaps 2;
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595 TGGAGCCTGTGGAAAGCGTGGAGTCTCAGTAGGTGCGCAAGGCCATCCTGGAGTGAAGTCT 654
661 ACCTCTTCCAGGGGCACTGGACACTCAGCAGAACTCGGTGGCTGTGGAGCAAGTCTT 720
655 GTCTCTTCCAACTCTGTGGACACTCATTCAGAGGTAGACTATCTTCAGGAGATCTCTT 714
721 CTTGGATTAAAGGAACAGCGCATCTCTTCAATTCAGAAAGTCCACGAGGAAAGAGAGT 780
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835 TTCTCCCAATCAGATCTGTAGCTCTTCCAAAGGGAACATGTTGAATCTGTAGAGCC 894
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895 AGGAGATTAGCCAGTCACTGGCCATTCTCTTAGGGGTCTTGTCTGTGTGGCTCCA 954
961 TATTGCTGTTCACAAATGTTCTTCAACTTATCGCAGAGGGGAGCGCCCAATCGATT 1020
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RESULT 13

US-10-272-983-13
; Sequence 13, Application US/10272983
; Publication No. US20030148450A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/10/272,983
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US/09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439

; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-272-983-13

Query Match 56.9%; Score 669; DB 6; Length 1173;

Best Local Similarity 74.2%; Pred. No. 2.2e-202; Indels 9; Gaps 2;
Matches 875; Conservative 0; Mismatches 295;

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Qy 181 GACTTCTTCTGGGTGTCTCTCCATTCCTCTGTGTACATCCCTCACAGCTGTTTAACTGG 240
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; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/10/393,807
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: US/09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
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; PRIOR FILING DATE: 1999-03-12
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; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; Remaining Prior Application data removed - See File Wrapper
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-393-807-13

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Query Match	56.9%	Score 669	DB 6	Length 1173
Best Local Similarity	74.2%	Pred. No. 2.2e-202		
Matches 875	Conservative 0	Mismatches 295	Indels 9	Gaps 2
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Qy	421	ATACTGGCTTTCTTGGTCAATGGGCCCAATGAATCTGGCTTCGGATTTCTTGAAGAACAGC	480	
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Qy	481	ACCAACACAGAGGATGGCGCTGGCTTGTGTTACTGAGTGGTATCATCTCTGCCCATTAACA	540	
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	268.4	22.8	1326	14	US-11-241-956-19 Sequence 19, Appl
2	138	11.7	2761	11	US-11-036-196-2003 Sequence 2003, Ap
3	138	11.7	2761	11	US-11-036-196-2003 Sequence 3990, Ap
4	133.6	11.4	2824	14	US-11-136-527-3990 Sequence 127, App
5	79.8	6.8	2483	14	US-11-136-527-2847 Sequence 2847, Ap
6	74	6.3	1401	14	US-11-127-877-4 Sequence 4, Appli
7	66.6	5.7	2348	14	US-11-136-527-3691 Sequence 3691, Ap
8	66.6	5.7	2348	14	US-11-036-196-1495 Sequence 1495, Ap
9	66.6	5.7	4095	14	US-11-136-527-2030 Sequence 2030, Ap
10	66.6	5.7	2633	14	US-11-136-527-3114 Sequence 3114, Ap
11	60.6	5.2	2733	14	US-11-136-527-2435 Sequence 2435, Ap
12	59.6	5.1	2699	14	US-11-127-877-5 Sequence 5, Appli
13	56.4	4.8	1773	14	US-11-127-877-17 Sequence 17, Appl
14	56.4	4.8	1974	14	US-11-124-368A-14 Sequence 14, Appl
15	54.8	4.7	600	14	US-11-136-527-7845 Sequence 7845, Ap
16	54.8	4.7	1269	14	US-11-136-527-3749 Sequence 3749, Ap
17	54.2	4.6	2146	8	US-10-750-185-35936 Sequence 35936, A
18	54.2	4.6	2146	8	US-10-750-623-35936 Sequence 35936, A

19	51.2	4.4	3741	14	US-11-136-527-751	Sequence 751, App
20	50.2	4.3	1400	14	US-11-136-527-4223	Sequence 4223, Ap
21	50.2	4.3	1400	14	US-11-136-527-8086	Sequence 8086, Ap
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24	47.6	4.0	1038	11	US-11-217-710-5	Sequence 5, Appli
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27	43.8	3.7	1303	14	US-11-128-061-570	Sequence 570, App
28	43.8	3.7	1303	14	US-11-128-049-570	Sequence 570, App
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C 30	43.6	3.7	197241	11	US-11-114-798-47	Sequence 47, Appl
C 31	42.6	3.6	6501	14	US-11-136-527-3427	Sequence 3427, Ap
C 32	42.4	3.6	706	8	US-10-750-185-32790	Sequence 32790, A
C 33	42.4	3.6	706	8	US-10-750-623-32790	Sequence 32790, A
C 34	42.4	3.6	1928	14	US-11-136-527-3095	Sequence 3095, Ap
35	42.4	3.6	2509	14	US-11-136-527-3738	Sequence 3738, Ap
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37	42	3.6	1056	14	US-11-174-816-4	Sequence 4, Appli
38	42	3.6	1056	14	US-11-174-751-5	Sequence 5, Appli
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40	41	3.5	2809	14	US-11-136-527-2036	Sequence 2036, Ap
41	40.6	3.5	1116	14	US-11-216-610-5	Sequence 5, Appli
42	40.6	3.5	1193	14	US-11-216-610-3	Sequence 3, Appli
43	40.6	3.5	1689	14	US-11-216-610-1	Sequence 1, Appli
44	40.6	3.5	1915	14	US-11-068-686-3	Sequence 3, Appli
45	40.6	3.5	1945	14	US-11-127-877-27	Sequence 27, Appl

ALIGNMENTS

RESULT 1
US-11-241-956-19
; Sequence 19, Application US/11241956
; Publication No. US20060024792A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS INC.; BAUGHN, Mariah R.;
; APPLICANT: GAUL Richard C.; CHAWLA, Narinder K.;
; APPLICANT: GANDHI, Ameena R.; HAFALIA, April J.A.;
; APPLICANT: RAMKUMAR, Javataxmi; TRIBOULEY, Catherine M.;
; APPLICANT: THORNTON, Michael B.; KALLICK, Deborah A.;
; APPLICANT: YAO, Monique G.; ELLIOTT, Vicki S.;
; APPLICANT: BURFORD, Neil; KHAN, Farrah A.;
; APPLICANT: YUE, Henry; LU, Yan;
; APPLICANT: ARVIZU, Chandra S.; ROOPA, Reddy M.;
; APPLICANT: NGUYEN, Daniel B.; LEE, Ernestine A.;
; APPLICANT: LU, Dyung Aina M.; ISON, Craig H.;
; APPLICANT: WALSH, Roderick T.; POLICKY, Jennifer L.
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: PI-0236 USN
; CURRENT APPLICATION NUMBER: US/11/241,956
; CURRENT FILING DATE: 2005-10-04
; PRIOR APPLICATION NUMBER: US/10/398,036
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: PCT/US01/30661
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/245,855
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/242,322
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 60/240,589
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US 60/249,343
; PRIOR FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: US 60/247,587
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/245,900
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/242,223
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 60/236,546
; PRIOR FILING DATE: 2000-09-29

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; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PERL Program
; SEQ ID NO 19
; LENGTH: 1326
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7474823CB1
US-11-241-956-19

Query Match          22.8%; Score 268.4; DB 14; Length 1326;
Best Local Similarity 77.8%; Pred. No. 7.8e-67;
Matches 339; Conservative 0; Mismatches 91; Indels 6; Gaps 1;

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QY 767 AGCGTGAATCACTCAG 782

RESULT 2
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; Sequence 2003, Application US/11036196
; Publication No. US20060078900A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Higgs, Brandon
; APPLICANT: Castle, Arthur
; APPLICANT: Elashoff, Michael
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5089-US
; CURRENT APPLICATION NUMBER: US/11/036,196
; CURRENT FILING DATE: 2005-01-18
; PRIOR APPLICATION NUMBER: US/10/152,319
; PRIOR FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: US 60/292,335
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/297,523
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,925
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,810
; PRIOR FILING DATE: 2001-07-10

; NUMBER OF SEQ ID NOS: 60/303,807
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/303,808
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/315,047
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: US 60/324,928
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US 60/330,867
; PRIOR FILING DATE: 2001-11-01
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2221
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2003
; LENGTH: 2761
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. NM_053506
US-11-036-196-2003

Query Match          11.7%; Score 138; DB 11; Length 2761;
Best Local Similarity 55.0%; Pred. No. 5.7e-29;
Matches 317; Conservative 0; Mismatches 250; Indels 9; Gaps 2;

QY 51 CTTGGCATTTTAAATGTCCTCTGCTTTTGTCTAATAGCATAGGCAATGCTGTGTCAT 110
Db |||||
QY 445 CTTGGCTGGCTCATGGCGCTGCTCATCTGGGCCACAGTACTGGGCAACGGCTGTGTCAT 504
QY 111 TTTAGCCTTTGTAGCAGACAGAAACCTTAGACATCGAAGTAATATATTTTCTTAAATTT 170
Db |||||
QY 505 GCTGCGCTTCGTGGCGGATTCGAGCCTCGGCCACCCAGAAACAATCTTCTTCTGCTCAACCT 564
QY 171 GGTATTTCTGACTTCTTGGTGTGTCATCTCCATCTCTCTGATACCTCCCTCACACGCT 230
Db |||||
QY 565 CGCCATCTCCGACTTCTCTGCTGGTGGCTTCTGTCATCTCCATTTGTCATCTGTCATCT 624
QY 231 GTTTAAAC---TGGAAATTTTGGAAATGGAATCTGCAATGTTTGGCTCATTTACTGACTATCT 287
Db |||||
QY 625 GACCGGCGCTTGGACCTTGGCGGGGCTCTGCAAGCTGTGGCTGGTGGTAGACTACCT 684
QY 288 TTTGTGCACAGCATCGCTCTACAGTATTTCTCTCATTTAGTACGATCGATACAGTCACT 347
Db |||||
QY 685 ACTGTGTGCTCTCTGCTCTTCAACATCTGATCTCATGATGATGACCGATTTCTGTCAGT 744
QY 348 TTCAAACGCTGTGCGTTATAGAGCACAGCACACTGTCATCTCGAAATTTGTTGCTCAAAAT 407
Db |||||
QY 745 CACTCGAGCTGTCTCTTACAGGGCCAGCAGGGGGGACAGAGACGGGCGCTTCGGAAGAT 804
QY 408 GGTGGCTGTTTGGATACTGGCTTCTTGTGTCATGTCCTCAATGGCCCAATGATTTCTGGCTTCGGAT-- 465
Db |||||
QY 805 GGCACCTGGTGTGGTGTGCTGGCTTCTGCTGTATGGGCTTGCCATCTCTGATGGGAGTA 864
QY 466 ----TCTTGGAAAGAACAGACCAACACAGAGAGTGGAGCCTTGGCTTGTGTTACTGAGTG 521
Db |||||
QY 865 CTTGCTGGTGGCAGTTCCATCCCGAGGGCCACTGCTATGCTGAGTCTTCTTACAACTG 924
QY 522 GTACATCTCGCCATTTACAGCATTTCTTGGAAATTTCTGCTCCCTGCTCTCTTGGTGTCTA 581
Db |||||
QY 925 GTACTTTTCTCATCAGGCTTCCACCTCGAGTTCTTACGGCCCTTCTCAGCGCTTCTCAGCGCTTACCTT 984
QY 582 TTTCAAGTGTACAGATTTTACTTGGAGCCTGTGGAGCG 617
Db |||||
QY 985 CTTCAACCTCAGCATCTACTCTGNACATCCAGAGCG 1020

RESULT 3
US-11-136-527-3990
; Sequence 3990, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
```


; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; PRIOR FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3990
; LENGTH: 2814
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-3990

Query Match 11.7%; Score 138; DB 14; Length 2814;
Best Local Similarity 55.0%; Pred. No. 5.7e-29;
Matches 317; Conservative 0; Mismatches 250; Indels 9; Gaps 2;
Qy 51 CTTGGCATTTTTAATGTCCTGCTTGTCTTGTCTATACGATAGGCAATGCTGGTGCAT 110
Db 435 CTTGGCTGGCTCATGGCGTCTCATCGTGGCCACAGTACTGGGCAACGGCTGGTGCAT 494
Qy 111 TTAGACCTTTGTAGCAGACAGAAACCTTAGACATCGAAGTAATTAATTTTCTTAATTT 170
Db 495 GCTCGCCTTGTGGCGGATTCGAGCCTCCGACCACGACAACTTCTTCTGCTCAACCT 554
Qy 171 GGCTATTCTGACTTCTTGGTGGGTGTCATCTCCATCTCTGTACATCCCTCACAGCT 230
Db 555 CGCCATCTCGACATCTCTCGTGGGTGCTTCTGATCCCATCCATTTGACGTACCTATGCT 614
Qy 231 GTTTAAC---TGGAAATTTTGGAAATGGAATCTGATGTTGGTCAATTAAGTACTATCT 287
Db 615 GACCGCGCTTGGACCTTCGCGCGGGGCTCTGCAAGCTGTGGTGGTAGACTACCT 674
Qy 288 TTGTGACAGCATCCGCTTACAGTATTGTCTCATTAAGCTACGATACGATACCACTCAGT 347
Db 675 ACTGTGGCTCTCTCGCTTCAACATCGTACTCATCAGTATACCGATTCCTGTGCTCAGT 734
Qy 348 TTCAAACGCTGTGGTGTATAGACACAGACACATCGGCATCTGAAATTTGTGCTCAAT 407
Db 735 CACTCGAGCTGTCTCTACAGGGCCAGAGGGGGACACAGAGCGGCGCTTCGGAAGAT 794
Qy 408 GGTGGCTGTTGGATCTGCTTCTTGGTCAATGGGCCCAATGATTCGTGCTTCGGAT-- 465
Db 795 GGCACTGGTGGGTGCTGGCTTCTCTGCTGATGGGCCCTGCCATCTGAGTTGGGAGTA 854
Qy 466 ----TCTTGAAGAACAGCACACAGAGGAGTGGAGCTTGGCTTGTACTGAGTG 521
Db 855 CCTGTCTGGTGGCAGTTCATCCCGAGGGCCACTGCTATGCTGAGTTCTTCTACAAGTG 914
Qy 522 GTACATCTCGCCATTAACAGCATTTTGGAAATTCCTGCTCCCTGCTCTCTTGGTGGTCTA 581
Db 915 GTACTTTCTCATCAGGCTCCACCTCGAGTTCTTCAAGCCCTTCTCAGCGTTACCTT 974
Qy 582 TTTCAGTGTACAGATTTACTGGAGCCTGTGGAAGCG 617
Db 975 CTTCAACCTCAGCATCTACCTGAACATCCAGAGCG 1010

RESULT 4
US-11-136-527-127
; Sequence 127, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; PRIOR FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830

; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 127
; LENGTH: 2824
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-127

Query Match 11.4%; Score 133.6; DB 14; Length 2824;
Best Local Similarity 52.1%; Pred. No. 1.1e-27;
Matches 300; Conservative 19; Mismatches 248; Indels 9; Gaps 2;
Qy 51 CTTGGCATTTTTAATGTCCTGCTTGTCTTGTCTATACGATAGGCAATGCTGGTGCAT 110
Db 445 CTTGGCTGGCTCATGGCGTCTCATCGTGGCCACAGTACTGGGCAACGGCTGGTGCAT 504
Qy 111 TTAGACCTTTGTAGCAGACAGAAACCTTAGACATCGAAGTAATTAATTTTCTTAATTT 170
Db 505 GCTCGCCTTGTGGCGGATTCGAGCCTCCGAGCCWCSRSRCSGMACRWCTMKTKTCKWCAASCT 564
Qy 171 GGCTATTCTGACTTCTTGGTGGGTGTCATCTCCATCTCTGTACATCCCTCACAGCT 230
Db 565 YRSNAKCTSGAKWKSSTCGTGGTGGCTTCTGATCCCATTTGACGTACCTATGCT 624
Qy 231 GTTTAAC---TGGAAATTTTGGAAATGGAATCTGATGTTGGTCAATTAAGTACTATCT 287
Db 625 GACCGCGCTTGGACCTTCGCGCGGGGCTCTGCAAGCTGTGGTGGTAGACTACCT 684
Qy 288 TTGTGACAGCATCCGCTTACAGTATTGTCTCATTAAGCTACGATACGATACCACTCAGT 347
Db 685 ACTGTGGCTCTCTCGCTTCAACATCGTACTCATCAGCTATGACCGATTCTGTGCTCAGT 744
Qy 348 TTCAAACGCTGTGGTGTATAGACACAGACACATCGGCATCTGAAATTTGTGCTCAAT 407
Db 745 CACTCGAGCTGTCTCTACAGGGCCAGAGGGGGACACAGAGCGGCGCTTCGGAAGAT 804
Qy 408 GGTGGCTGTTGGATCTGCTTCTTGGTCAATGGGCCCAATGATTCGTGCTTCGGAT-- 465
Db 805 GGCACTGGTGGGTGCTGGCTTCTCTGCTGATGGGCCCTGCCATCTGAGTTGGGAGTA 864
Qy 466 ----TCTTGAAGAACAGCACACAGAGGAGTGGAGCTTGGCTTGTACTGAGTG 521
Db 865 CCTGTCTGGTGGCAGTTCATCCCGAGGGCCACTGCTATGCTGAGTTCTTCTACAAGTG 924
Qy 522 GTACATCTCGCCATTAACAGCATTTTGGAAATTCCTGCTCCCTGCTCTCTTGGTGGTCTA 581
Db 925 GTACTTTCTCATCAGGCTCCACCTCGAGTTCTTCAAGCCCTTCTCAGCGTTACCTT 984
Qy 582 TTTCAGTGTACAGATTTACTGGAGCCTGTGGAAGCG 617
Db 985 CTTCAACCTCAGCATCTACCTGAACATCCAGAGCG 1020

RESULT 5
US-11-136-527-2847
; Sequence 2847, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; PRIOR FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2847
; LENGTH: 2483
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-2847

Query Match 6.8%; Score 79.8; DB 14; Length 2483;
Best Local Similarity 55.3%; Pred. No. 3.7e-12;
Matches 172; Conservative 2; Mismatches 134; Indels 3; Gaps 1;

QY 73 CTTGCTTTTGTCTAATAGATAGGCAATGCTGTGTCATTTTATAGCCTTTGTAGCAGACAGA 132
DB 548 CTCAGTCTGTGACCATCATTTGGGAACATTTCTGTCATGTTTCCATTAAAGTCARCCGC 607
QY 133 AACCTTAGACATCGAAGTAATTTTCTTAAATTTGGCTATTTCTGACTTCTTCGTG 192
DB 608 CACCTTCAGACTGTCAACAATTAATTTCTGTCAGCTGGCCCTGTGCTGACCTCATCATTA 667
QY 193 GGTGTCATCTCCATTCCTCTGTATACCTCCCTCACAGCTGTTT---AACTGGAATTTTGA 249
DB 668 GGTGTTTCTCCATGAACTGTATACCTCTACACTGTGATTTGGCTACTGGCCCTTTGGGA 727
QY 250 AGTGAATCTGCATGTTTGGCTCATTAATGACTATCTTTTGTGACAGCATCCGCTCTAC 309
DB 728 CCTGTAGTATGTGACCTTTGGCTAGCATTTGGACTATGTTGTACAGCAATGCTCCGTTATG 787
QY 310 AGTATTGCTCTCATTAAGTACGATCGATACCACTGCTGATTTCAACGCTGTGCGTTATAGA 369
DB 788 AATCTCTCATCATCAGCTTTGTATAGATATCTTCTGTGTACGAAACCTCTGACCTACCCA 847
QY 370 GCACAGCACAC 380
DB 848 GTTAAGCGGAC 858

RESULT 6
US-11-127-877-4
; Sequence 4, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; TITLE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 1401
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-4

Query Match 6.3%; Score 74; DB 14; Length 1401;
Best Local Similarity 53.1%; Pred. No. 1.3e-10;
Matches 205; Conservative 0; Mismatches 175; Indels 6; Gaps 2;

QY 73 CTTGCTTTTGTCTAATAGATAGGCAATGCTGTGTCATTTTATAGCCTTTGTAGCAGACAGA 132
DB 97 CTCAGTTTGTGACCATTAATTCGGGAACATCTAGTCATGTTTCCATTAAAGTCARCCGC 156
QY 133 AACCTTAGACATCGAAGTAATTTTCTTAAATTTGGCTATTTCTGACTTCTTCGTG 192
DB 157 CACCTCCAGACCGCTCAACAATTAATTTTATTCAGCTTTGGCCCTGTGCTGACCTTATCATTA 216
QY 193 GGTGTCATCTCCATTCCTCTGTATACCTCCCTCACAGCTGTT---TAACCTGGAATTTTGA 249
DB 217 GGTGTTTCTCCATGAACTTTGTACCCCTCTACACTGTGATTTGGTTACTGGCCCTTTGGGA 276
QY 250 AGTGAATCTGCATGTTTGGCTCATTAATGACTATCTTTTGTGACAGCATCCGCTCTAC 309

DB 277 CCTGTGGTGTGTGACCTTTTGGCTAGCCCTGGACTATGTGGTCAGCAATGCCCTCAGTTATG 336
QY 310 AGTATTGTCTCTCATTAGCTACGATACGATACCACTAGTTTCAAAACGCTGTGCGTTATAGA 369
DB 337 AATCTGCTCATCATCAGCTTTGACAGGTACTTCTGTGTCAAAAACCTCTGACCTACCCA 396
QY 370 GCACAGCACATGGCATCCTGAAATTTGTGCTCAAAATGGTGGCTTTTGGATACTGGCT 429
DB 397 GTCAGCGGACCAAAAATGGCA---GGTATGATGATTTGCAGCTGCCCTGGGTCTCTCT 453
QY 430 TTCTTGGTCAATGGGCCCAATGATTCT 455
DB 454 TTCAATCTCTGGGCTCCAGCCATTCT 479

RESULT 7
US-11-136-527-3691
; Sequence 3691, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3691
; LENGTH: 2348
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-3691

Query Match 5.7%; Score 66.6; DB 14; Length 2348;
Best Local Similarity 52.3%; Pred. No. 2.3e-08;
Matches 172; Conservative 0; Mismatches 154; Indels 3; Gaps 1;

QY 46 GTCCCTTGGCATTTTAAATGTCCTGCTGCTTTGCTATACGATAGCATGCTGTG 105
DB 333 GTCTTCAATGCTCTTCTTAAACCGCTTCTCTGGCATTTGGTCAACATCATCCCTT 392
QY 106 GTCAATTTTAGCCCTTTGTAGCAGACAGAAACCTTAGACATCGAAGTAATTTTCTT 165
DB 393 GTCAATTTGGCTTTCAAGTCAACAACAGCTCAACACTACTTCTCTT 452
QY 166 AATTTGGCTATTTCTGACTTCTTTCGGGTGTCATCTCCATTCCTCTGTACATCCCTAC 225
DB 453 AGCTGGCTGTGACAGACCTGATCATCGGGGTCAATTTCCATGAACCTGTTCACCTAC 512
QY 226 AGCTGTTTAAAC---TGGAAATTTGGAAGTGGATCTGATTTGCTGCTTATGCTGCTTAC 282
DB 513 ATCAATTAAGAACCGTTGGGCACTGGGGAACCTTAGCCTGGGACCTCTGGCTCTCCATTTGAC 572
QY 283 TATCTTTTGTGACAGCATCCGCTCTACAGTATTTGCTCTCAATAGCTACGATCGATACCA 342
DB 573 TATGTGGCAGCAANTGCCCTCTGTCAATGATCTGCTGTCTATGAGCTTTGACAGGTACTTT 632
QY 343 TCAGTTTCAAAACGCTGTGCTTATAGAGC 371
DB 633 TCCATCACTAGGCCCACTCACTACCGAGC 661

RESULT 8
US-11-036-196-1495
; Sequence 1495, Application US/11036196
; Publication No. US20060078900A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory

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RESULT 10
US-11-136-527-3114
; Sequence 3114, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3114
; LENGTH: 2633
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-3114

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QY 129 CAGAAACCTTAGACATCGAAGTAATATATTTTCTTAATTTGGCTATTTCGACTCTT 188
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 305 CACCGAGCTCAAGACAGTCAACAATCTTCTGCTGAGCTGGCTGCTGACCTCAT 364
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 189 CGTGGGTGTCATCTCCATCTCTGTACATCCCTCACACGCTGTTTA---ACTGGAATTT 245
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 365 CATTTGGCACCTTCTCCATGAACCTCTATACACGATACCTGCTCATGGGCCACTGGGCTCT 424
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 246 TGGAAAGTGGAACTGCGATGTTTGGCTCATTTACTGACTATCTTTTGTGCACAGCATCCGT 305
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 425 GGGCACACTGGCTGTGACCTCTGGCTGGCCCTGGACTATGTGGCAGACAGCCCTCTGT 484
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 306 CTACAGTATTGCTCTCATTTAGCTACGATCGATCCAGTCTCAGTTTCAAACGCTGTGCGTTA 365
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 485 CATGAATCTTCTGCTCATCAGCTTTGACCGTTACTTCTCGGTGACCGCCCTGAGCTA 544
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 366 TAGAGCACAGCACT 381
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 545 CCGAGCCAGCGCACT 560
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 11
US-11-136-527-2435
; Sequence 2435, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 2435
; LENGTH: 2733
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-2435

Query Match 5.2%; Score 60.6; DB 14; Length 2733;
Best Local Similarity 51.1%; Pred. No. 1.4e-06;
Matches 169; Conservative 0; Mismatches 159; Indels 3; Gaps 1;

QY 53 TGGCATTTTAAATGCTCCCTGCTTCTTCTATACGATAGGCAATGCTGGTCAATTT 112
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1068 TTGCAGTTGTGACTGGCGGTGCTCAGCCTGATGACCAATGTTCGGCAATGTCTTGGTCATGA 1127
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 113 TAGCCTTTGTAGCAGACAGAAACCTTAGACATCGAAGTAATATTTTCTTAATTTGG 172
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1128 TCTCCTTCAAAGTCAACAGTCAAGTCAAGACAGTTAACTACTACCTGCTCAGCTGG 1187
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 173 CTATTTCTGACTTCTTCTGGGTGTCATCTCCATTCCTCTGTATCATCCCTCACACGCTGT 232
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1188 CCTGTGCAGACCTCATCATTTGGCATCTTCTCCATGAACCTCTACACGACCTACATCTCA 1247
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 233 TTTAA---CTGGAATTTTGGAAATCTGCAATGTTTGGCTCATTTACTGACTATCTTT 289
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1248 TGGGACGCTGGGTTCTCGGAGTCTGGCTTTGTGACCTTTTGGCTGGCACCTGCACTATGTAG 1307
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 290 TGTGCAAGACTCGTCTACAGATTCTGCTCATTTAGCTACGATCGATACAGTCACTTT 349
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1308 CCAGCAATGCTTCTGTCATGAACCTCTCGGTGATTAGTTTGTGTTACTTTTCCATCA 1367
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 350 CAAACGCTGTGCGTTATAGACACAGCAC 380
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1368 CAAGACCACTGACCTACCGGGCCAGCGGTAC 1398
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 12
US-11-127-877-5
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; Sequence 5, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 5
; LENGTH: 2699
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-5

Query Match 5.1%; Score 59.6; DB 14; Length 2699;
Best Local Similarity 50.6%; Pred. No. 2.6e-06;
Matches 171; Conservative 0; Mismatches 164; Indels 3; Gaps 1;

QY 47 TCCCTTGGCATTTTAAATGCTCCCTGCTTCTTCTATACGATAGGCAATGCTGTGG 106
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 406 TCACCATTCGAGCTGTGACTGTGTGAAGCTGTATCACCATTGTGGGCAATGCTGTGG 465
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 107 TCATTTTAGCTTTGTAGCAGACAGAAACCTTAGACATCGAAGTAATATTTTCTTTA 166
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 466 TCATGATCTCTTCAAAGTCAACAGCCAGCTCAAGACAGTTAACTATTACCTGTCA 525
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 167 ATTTGGCTATTCTGACTTCTTCTGGGTGTCATCTCCATTCCTCTGATACGATCCCTCA 226
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 526 GCTTAGCCTGTGAGATCTCATTTGGAATCTTCTCCATGAACCTCTACACCACTACA 585
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 227 CGCTGTTTAA---CTGGAATTTTGGAGTGAATCTGCATCTTTCGCTCATTTACTGACT 283
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 586 TCCTCATGGAGCTGGGCTCTCGGAGTCTGGCTTGTGACCTTTGGCTTGGCACTGACT 645
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 284 ATCTTTTGTGCAAGCATCCGCTACAGATATTCTCTCATTTAGCTACGATCGATACCACT 343
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Db 646 ACCTGCCAGCAAGCTTCTGTGATGAACCTTCTGGTGAATCACTTTTGACCGTTACTTTT 705
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QY 344 CAGTTTCAAACGCTGTGCGTTATAGACACAGCACACT 381
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Db 706 CCATCAAGACCTTGAATATCGGGCCAAAGCGTACT 743
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RESULT 13
US-11-127-877-17
; Sequence 17, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: Patent in version 3.3
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; SEQ ID NO 17
; LENGTH: 1773
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-127-877-17

Query Match      4.8%; Score 56.4; DB 14; Length 1773;
Best Local Similarity 50.0%; Pred. No. 1.8e-05;
Matches 169; Conservative 0; Mismatches 166; Indels 3; Gaps 1;

Qy 46 GTCCCTTGGCAATTTTAAGTCCCTGCTGCTTTGCTATTAAGATAGGCAATGCTGTG 105
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
205 GTCTTCATCGCTTCTTAAACGGGCATCTGGGCTTGGTGACCATCATCGGCAACATCTG 264
Qy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
106 GTCAATTTAGCCTTTGTAGCAGACAGAAACCTTAGACATCGAAGTAATATTTTCTT 165
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
265 GTAAATGTGTCAATTTAAGGTCAACAGCAGCTGAAGACGGGTCAACAACTACTTCTCTTA 324
Qy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
166 AATTTGGCTATTTCTGACTTCTCGTGGGTGCTATCTCCATTCTCTGTACATCCCTCAC 225
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
325 AGCTGGCTGTGCGGATCTGAATATCGGGTCAATTTCAATGAATCTGTTTACGACCTAC 384
Qy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
226 ACCTGTTTAAAC---TGGAAATTTTGAAGTGGAAATCTGCATGTTTGGCTCATTACTGAC 282
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
385 ATCATCATGAATCGATGGCCCTTAGGGAACCTTGGCCTGTGACCTCTGGCTTGCCATTGAC 444
Qy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
283 TATCTTTTGTGACAGATCCGCTCTACAGTATGCTCTCATTTAGCTAGCATCGATCGATACAG 342
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
445 TACGTAGCCAGCAATGCTCTGTTATGAATCTTCTGGTCTATCAGCTTTGACAGATACTTT 504
Qy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
343 TCAGTTTCAAACGCTGTGCGTTATAGACACAGACACAC 380
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
505 TCCATCAGAGCGCGCTCACGTACCGAGCCAAACGAAC 542

RESULT 14
US-11-124-368A-14
; Sequence 14, Application US/11124368A
; Publication No. US20050287559A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: James J. Devlin
; APPLICANT: May Luke
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof
; FILE REFERENCE: CL001524
; CURRENT APPLICATION NUMBER: US/11/124.368A
; PRIOR FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,845
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/625,936
; PRIOR FILING DATE: 2004-11-09
; NUMBER OF SEQ ID NOS: 21112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 1974
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-124-368A-14

Query Match      4.8%; Score 56.4; DB 14; Length 1974;
Best Local Similarity 50.0%; Pred. No. 1.9e-05;
Matches 169; Conservative 0; Mismatches 166; Indels 3; Gaps 1;

Qy 46 GTCCCTTGGCAATTTTAAGTCCCTGCTGCTTTGCTATTAAGATAGGCAATGCTGTG 105
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
205 GTCTTCATCGCTTCTTAAACGGGCATCTGGGCTTGGTGACCATCATCGGCAACATCTG 264
Qy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
106 GTCAATTTAGCCTTTGTAGCAGACAGAAACCTTAGACATCGAAGTAATATTTTCTT 165
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
265 GTAAATGTGTCAATTTAAGGTCAACAGCAGCTGAAGCGGTCAACAACTACTTCTCTTA 324
Qy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
166 AATTTGGCTATTTCTGACTTCTCGTGGGTGCTATCTCCATTCTCTGTACATCCCTCAC 225
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325 AGCTGGCTGTGCGGATCTGAATATCGGGTCAATTTCAATGAATCTGTTTACGACCTAC 384
Qy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
226 ACCTGTTTAAAC---TGGAAATTTTGAAGTGGAAATCTGCATGTTTGGCTCATTACTGAC 282
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
385 ATCATCATGAATCGATGGGCTTAGGGAACCTTGGCCTGTGACCTCTGGCTTGCCATTGAC 444
Qy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
283 TATCTTTTGTGACAGACATCGCTCTACAGTATGCTCTCATTTAGCTAGCATCGATCGATACAG 342
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
445 TACGTAGCCAGCAATGCTCTGTTATGAATCTTCTGGTCTATCAGCTTTGACAGATACTTT 504
Qy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
343 TCAGTTTCAAACGCTGTGCGTTATAGACACAGACACAC 380
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
505 TCCATCAGAGCGCGCTCACGTACCGAGCCAAACGAAC 542

RESULT 15
US-11-136-527-7845
; Sequence 7845, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7845
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-7845

Query Match      4.7%; Score 54.8; DB 14; Length 600;
Best Local Similarity 51.7%; Pred. No. 3.1e-05;
Matches 125; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

Qy 884 TGGAGCTTCTCAGAGGCGAGGAAGCTAGCCAGGTGCTAGCTGCTCTGAGTGTCTTTG 943
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
335 TGGCTTGGCCCGTGAAGGAGAGCGTGAAGACTCTGGGCATCATCATGCGCACCTTCA 394
Qy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
944 CCATTTCTGGGCTCCGTTATTTGCTGTTCACAAATGTTTCTTCAACTTATCGCAGAGGG 1003
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
395 TCCTCTGCTGGCTGCGCTTTTTCATTGCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTG 454
Qy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1004 AGGCCCCCAATCGATTTGGTACAGATAGCCTTTTGGCTTACAGTGGTTCAATTCACCTTA 1063
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
455 GCCACATGCTGCGTTGTTGGGTGCCATAATTAACCTGGCTAGGCTACTCCAACTCCCTGC 514
Qy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1064 TTAATCCCTTTCTATACCTTTTGGCCACAGAGCTTTCCAGAGGCTTTCTTGGGAAGATAC 1123
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
515 TCAATCCGGTTATTATGCTTATTTCACAAAGAGCTTTTCAAAACGCTTTTAAAGAGATAA 574
Qy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1124 TC 1125
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
575 TC 576

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Job time : 690 secs
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Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 26, 2006, 20:46:57 ; Search time 27 Seconds
(without alignments)

Title: US-10-626-126-9
Perfect score: 2045
Sequence: 1 MSENGTDVLEPLTAQVPIAF.....WKILCVTKQAPAPSQTSQSVSS 391

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgm2_6/pdata/1/iaa/PCURS_COMB.pep.*
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6: /cgm2_6/pdata/1/iaa/backfiles1.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	1403.5	68.6	390	2	US-09-414-010-2	Sequence 2, Appli
2	1403.5	68.6	390	2	US-09-812-216-2	Sequence 2, Appli
3	1403.5	68.6	390	2	US-09-875-076-14	Sequence 14, Appli
4	698	34.1	445	2	US-10-453-106-2	Sequence 2, Appli
5	693	33.9	445	1	US-08-985-090-2	Sequence 2, Appli
6	693	33.9	445	2	US-09-165-543-2	Sequence 2, Appli
7	693	33.9	445	2	US-09-167-354-7	Sequence 7, Appli
8	693	33.9	445	2	US-09-642-855-7	Sequence 7, Appli
9	693	33.9	445	2	US-09-642-514-7	Sequence 7, Appli
10	693	33.9	445	2	US-09-642-852-7	Sequence 7, Appli
11	693	33.9	445	2	US-10-453-106-1	Sequence 1, Appli
12	693	33.9	449	2	US-09-949-016-10930	Sequence 10930, A
13	693	33.9	453	2	US-09-891-053-20	Sequence 20, Appli
14	690	33.7	413	2	US-09-891-053-1	Sequence 1, Appli
15	682	33.3	445	2	US-09-165-543-5	Sequence 5, Appli
16	682	33.3	445	2	US-09-891-053-25	Sequence 25, Appli
17	682	33.3	445	2	US-10-453-106-3	Sequence 3, Appli
18	617	30.2	351	2	US-09-524-162-2	Sequence 2, Appli
19	538	26.3	362	1	US-08-985-090-5	Sequence 5, Appli
20	538	26.3	362	2	US-09-165-543-32	Sequence 32, Appli
21	419	20.5	348	1	US-08-118-270-13	Sequence 13, Appli
22	419	20.5	348	4	PCR-US93-08528-13	Sequence 13, Appli
23	409.5	20.0	355	1	US-08-118-270-11	Sequence 11, Appli
24	409.5	20.0	355	4	PCR-US93-08528-11	Sequence 11, Appli
25	403.5	19.7	590	2	US-09-538-092-967	Sequence 967, App
26	400.5	19.6	410	2	US-09-721-870-177	Sequence 177, App
27	398.5	19.5	590	2	US-09-826-503-517	Sequence 517, App

28	397	19.4	479	1	US-08-313-553-7	Sequence 7, Appli
29	397	19.4	479	2	US-08-767-993-7	Sequence 7, Appli
30	395	19.3	532	2	US-09-826-509-521	Sequence 521, Appli
31	387.5	18.9	390	1	US-08-461-812-4	Sequence 4, Appli
32	387.5	18.9	390	1	US-08-157-185-15	Sequence 15, Appli
33	387.5	18.9	390	2	US-08-281-526B-15	Sequence 15, Appli
34	387.5	18.9	390	2	US-09-450-790A-15	Sequence 15, Appli
35	387.5	18.9	390	2	US-09-333-837-15	Sequence 15, Appli
36	387.5	18.9	390	2	US-09-371-705-4	Sequence 4, Appli
37	386.5	18.9	390	2	US-09-826-509-427	Sequence 427, Appli
38	382.5	18.7	398	1	US-08-370-542-6	Sequence 6, Appli
39	382.5	18.7	398	1	US-08-542-358-6	Sequence 6, Appli
40	382.5	18.7	398	2	US-09-018-331-6	Sequence 6, Appli
41	382.5	18.7	460	2	US-09-826-509-513	Sequence 513, Appli
42	379.5	18.6	354	1	US-08-313-553-9	Sequence 9, Appli
43	379.5	18.6	354	2	US-08-767-993-9	Sequence 9, Appli
44	379.5	18.6	390	1	US-07-817-920-6	Sequence 6, Appli
45	379.5	18.6	390	1	US-08-117-006-6	Sequence 6, Appli

ALIGNMENTS

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RESULT 1
US-09-414-010-2
; Sequence 2, Application US/09414010
; Patent No. 6204017
; GENERAL INFORMATION:
; APPLICANT: Behan, Jiang Xu
; APPLICANT: Hedrick, Joseph A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Monima, Frederick J. Jr.
; APPLICANT: Morse, Kelley L.
; APPLICANT: Umland, Shelby P.
; APPLICANT: Wang, Suke
; TITLE OF INVENTION: Histamine receptor
; FILE REFERENCE: CN01069
; CURRENT APPLICATION NUMBER: US/09/414,010
; CURRENT FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-414-010-2

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Query Match	68.6%	Score	1403.5	DB 2	Length	390			
Best Local Similarity	69.1%	Pred. No.	1.2e-112						
Matches	271	Conservative	40	Mismatches	78	Indels	3	Gaps	2

Qy	1	MSENGTDVLP	LTQAQVPLAF	MLMSLLAF	ITIGNAVVILAF	VAQDNTLRHRS	SYFFNLALIS	60	
Db	1	MPDNTSINLS	TRVTLTAFF	MSLVAFAL	MLGNALVILAF	VVDKNTLRHRS	SYFFNLALIS	60	
Qy	61	DFPVGVIS	PLXYIPHT	LENNPGSG	ICMFWLITD	YLCTASVVS	IVLISDYRQVS	NAV 120	
Db	61	DFPVGVIS	PLXYIPHT	LEFWDKB	ICVFWLITD	YLCTASVNV	IVLISDYRIVS	NAV 120	
Qy	121	RYRAQHTG	ILKIYAQ	VMVAVMILAF	LNGPMPILAS	DSWKNSNT	TECEPGFV	TEWYILAIT 180	
Db	121	SYRTQHTG	VKLIVTL	MVAVVWILAF	LNGPMPILIS	ESHWDEGS	--ECBPGFSE	WYILAIT 178	
Qy	181	AFLEFLLP	SVLVYFVS	QVIYWSL	KRGSLSR	CFSPHAGFIAT	SSRGTHSR	TGACRTSL 240	
Db	179	SFLFVIVP	ILVAVFNN	NIYWSL	WKRDHL	SRCQSHPG	LTVASSNI	CGHSPGR	LSSRSL 238
Qy	241	PGLEKPAAS	LHSSPRGK	SLVLSLR	THMSGSI	IAFKVGSFC	RSESPVLV	HQREHV	LLRG 300
Db	239	SASTEVPAS	PHSERQR	KSSLMFSS	RTKMSNT	IAKMGFS	QSDSVAL	HQREHV	LLRA 298
Qy	301	RKLARSLAV	LLSAPAC	WAPYCI	PTVILSV	TYRRGER	PKSITWYS	IAFWLQFNS	LINPLY 360

Db 299 RRLAKSLAILLGVFAVCWAPYSFTTIVLSFYSSATGPKSVVYRIAFWLQWNSFVNPLLY 358
Qy 361 PLCHRRFQKAFWKILCVTKQAPSO-TQS VSS 391
Db 359 PLCHKRFPQAKFLKIFCIKKQPLPSQHSRSVSS 390

RESULT 2
US-09-812-216-2
; Sequence 2, Application US/09812216
; Patent No. 6613533
; GENERAL INFORMATION:
; APPLICANT: Behan, Jiang Xu
; APPLICANT: Hedrick, Joseph A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Monsma, Frederick J. Jr.
; APPLICANT: Morse, Kelley L.
; APPLICANT: Umland, Shelby P.
; APPLICANT: Wang, Suke
; TITLE OF INVENTION: Histamine receptor
; FILE REFERENCE: CN01069
; CURRENT APPLICATION NUMBER: US/09/812,216
; CURRENT FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 09/414,010
; PRIOR FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-812-216-2

Query Match 68.6%; Score 1403.5; DB 2; Length 390;
Best Local Similarity 69.1%; Pred. No. 1.2e-112;
Matches 271; Conservative 40; Mismatches 78; Indels 3; Gaps 2;

Qy 1 MSESNGTDVLPITAOVPLAFMLSLAFAITIGNAVVILAFVADRNLRHRSNYFFFLNLALS 60
Db 1 MPTNSTINLSLSTRVTLAFFMSLVAFALMGNALVILAFVVDKDLHRSSYFFFLNLALS 60

Qy 61 DFFVGVISIPLYIPHTLFNPNPSSGICMFWLIIDYLLCTASVYSIVLISYDRYQSVNAV 120
Db 61 DFFVGVISIPLYIPHTLFNPNPSSGICMFWLIIDYLLCTASVYSIVLISYDRYQSVNAV 120

Qy 121 RYRAQHTGILKIVAQVAVWVILAFVNGPMILASDSKNSNTTECEPGFVTEWYILAIT 180
Db 121 SYRTOHTGVLKIVTLMAVAVVLAFLVNGPMILVSESWKDEGS--ECEPGFFSEWYILAIT 178

Qy 181 AFLEFLLPVSLVVYFSVQIYWSLWKRGSLSRCPFHAGFIATSSRGTGHSRRRTGLACTSL 240
Db 179 SFLEFVIPVLIVAFNNIYWSLWKRDHLSRCQSHPGLTAVSNNICGHSFRGLSRRSL 238

Qy 241 PGLKEPAASLHSPRGKSLLSVLRTHMSGSLIAFKVSGFCRSESPVLHQREHVLLRG 300
Db 239 SASTEPVAFHSPRRQRKSLMSSRTKWSNTIASKMGSPSQSDSVALHQREHVLLRA 298

Qy 301 RKLARSLAVLLSAPACWAPYCLFTTIVLSTYRRGERPKSIWYSIAFWLQWNSLNPFLY 360
Db 299 RRLAKSLAILLGVFAVCWAPYSFTTIVLSFYSSATGPKSVVYRIAFWLQWNSFVNPLLY 358

Qy 361 PLCHRRFQKAFWKILCVTKQAPSO-TQS VSS 391
Db 359 PLCHKRFPQAKFLKIFCIKKQPLPSQHSRSVSS 390

RESULT 3
US-09-875-076-14
; Sequence 14, Application US/09875076
; Patent No. 6869776
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.

; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/09/875,076
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,127
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,131
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/141,448
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/156,653
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,633
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,555
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,634
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/157,280
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,294
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,281
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,293
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,282
; PRIOR FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-875-076-14

Query Match 68.6%; Score 1403.5; DB 2; Length 390;
Best Local Similarity 69.1%; Pred. No. 1.2e-112;
Matches 271; Conservative 40; Mismatches 78; Indels 3; Gaps 2;

Qy 1 MSESNGTDVLPITAOVPLAFMLSLAFAITIGNAVVILAFVADRNLRHRSNYFFFLNLALS 60
Db 1 MPTNSTINLSLSTRVTLAFFMSLVAFALMGNALVILAFVVDKDLHRSSYFFFLNLALS 60

Qy 61 DFFVGVISIPLYIPHTLFNPNPSSGICMFWLIIDYLLCTASVYSIVLISYDRYQSVNAV 120
Db 61 DFFVGVISIPLYIPHTLFNPNPSSGICMFWLIIDYLLCTASVYSIVLISYDRYQSVNAV 120

Qy 121 RYRAQHTGILKIVAQVAVWVILAFVNGPMILASDSKNSNTTECEPGFVTEWYILAIT 180
Db 121 SYRTOHTGVLKIVTLMAVAVVLAFLVNGPMILVSESWKDEGS--ECEPGFFSEWYILAIT 178

Qy 181 AFLEFLLPVSLVVYFSVQIYWSLWKRGSLSRCPFHAGFIATSSRGTGHSRRRTGLACTSL 240

Db 179 SFLEFVPIVILVAYFNWNIYWSLWKRDHLSRCOSHFCGLTAVSSNICGHSFGRGLSSRRSL 238
Qy 241 PGLKEPAASHSSSPRGKSLLSVLTRHMSGSIAPKVGSCFCSSESPVTLHQREHVELLRG 300
Db 239 SASTEVPAFSPSRQRKRSKSLMFSRRTKMSNTIASKMGFSQSDSVLHQREHVELLRA 298
Qy 301 RKLARSIAVLSSPAICWAPCYCLPTTIVLSTYRGERPKSIWYSIAFWLQWFNLSLNPFLY 360
Db 299 RRLAKSLAILLGVFAVCWADYSUFTIVLSFYSSATGPKSVWYRIAFWLQWFNLSFVNPLLY 358
Qy 361 PLCHRFQKAFWKILCTKQAPSQ-TQSVSS 391
Db 359 PLCHRFQKAFKIFCLIKQPLSQHSRSVSS 390
RESULT 4
US-10-453-106-2
; Sequence 2, Application US/10453106
; Patent No. 6906060
; GENERAL INFORMATION:
; APPLICANT: Peschke, Bernd
; APPLICANT: Hohlweg, Rolf
; TITLE OF INVENTION: SUBSTITUTED HEXAHYDROPIRROLO[1,2-A]PYRAZINES,
; TITLE OF INVENTION: OCTAHYDROPIRROLO[1,2-A]PYRAZINES AND
; TITLE OF INVENTION: DECAHYDROPIRAZINO[1,2-A]AZEPINES
; FILE REFERENCE: 6483.200-US
; CURRENT APPLICATION NUMBER: US/10/453.106
; CURRENT FILING DATE: 2003-06-03
; PRIOR FILING DATE: 2002-06-07
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: Danish Application no. PA 2002 00863
; PRIOR FILING DATE: 2002-06-06
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Monkey
US-10-453-106-2

Query Match 34.1%; Score 698; DB 2; Length 445;
Best Local Similarity 37.8%; Pred. No. 5.8e-52;
Matches 165; Conservative 49; Mismatches 126; Indels 96; Gaps 11;
Qy 18 LAFMSLLAPAITIGNAVILAFVADNRNLRHRSNYFNLNLAISDPFVGVISIPLYIPTL 77
Db 37 LAALMALLIVATVGLGNALVMAFVADSSLRQTQNNFFLNLAISDFLVGAFCIPLYVPYL 96
Qy 78 F-NNPFGSGICMPWLITDYLLCTASVYSIVLISYDRYQSVSNVRAQHTGILKIVAOM 136
Db 97 TGRWTFGRGLCKLWLVVDYLLCTSSAFNIVLISYDRFLSVTRAVSYRAQQGNTTRAVRK 156
Qy 137 VAWIILAFVNGPMILASDWSK-----NSTNTECEPFGFVTEWYILAITAFLEFLPVSL 191
Db 157 LLVWVLAFLYLGPAIL---SWEYLSGGSSIPGHCYAEFPYNYFLITASTLEFFTPFLS 213
Qy 192 VYFVSQIY-----NSLWKGSLSRCPSH 215
Db 214 VTFNLSIYLNIOQRTRFLDLGAREAGPEPPPEAQPSPPPPGCGWCKGHEAMPLH 273
Qy 216 -----AGFIATSSRGTHSRRTGLACTSLPGLKEPAASHSSSPRGKSLLV 263
Db 274 RYGVGEAAVGAEGEATLGGGGGGGS-----AASPTSSG-----SSSRGTERPR----- 318
Qy 264 SLRTHMSGSIAPKVGSCFCSSESPVTLHQ-----EHVELLRGKRLARSIAVLSSAF 314
Db 319 -----SUKRGSKPSSASSLEKRMKMSVQSFTQRFRLSRDRKVAKSLAVISIF 367
Qy 315 AICWAPCYCLTIVLSTYRGERPKSIWYSIAFWLQWFNLSLNPFLYPLCHRRFQKAFWKI 374
Db 368 GLCWAPYLLMLITRAAC-HGHCVPDYWYETSFLLWANSVNPVLPCLCHHSFRFAFTKL 426

Qy 375 LCVTK---OPAPSQTQ 387
Db 427 LCPQKLIKQPHSSLEQ 442
RESULT 5
US-08-985-090-2
; Sequence 2, Application US/08985090
; Patent No. 5885893
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl
; TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,090
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jean M. Silveri
; REGISTRATION NUMBER: 39,030
; REFERENCE/DOCKET NUMBER: MNI-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 445 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-985-090-2

Query Match 33.9%; Score 693; DB 1; Length 445;
Best Local Similarity 37.6%; Pred. No. 1.6e-51;
Matches 163; Conservative 50; Mismatches 124; Indels 96; Gaps 11;
Qy 18 LAFMSLLAPAITIGNAVILAFVADNRNLRHRSNYFNLNLAISDPFVGVISIPLYIPTL 77
Db 37 LAALMALLIVATVGLGNALVMAFVADSSLRQTQNNFFLNLAISDFLVGAFCIPLYVPYL 96
Qy 78 F-NNPFGSGICMPWLITDYLLCTASVYSIVLISYDRYQSVSNVRAQHTGILKIVAOM 136
Db 97 TGRWTFGRGLCKLWLVVDYLLCTSSAFNIVLISYDRFLSVTRAVSYRAQQGNTTRAVRK 156
Qy 137 VAWIILAFVNGPMILASDWSK-----NSTNTECEPFGFVTEWYILAITAFLEFLPVSL 191
Db 157 LLVWVLAFLYLGPAIL---SWEYLSGGSSIPGHCYAEFPYNYFLITASTLEFFTPFLS 213
Qy 192 VYFVSQIY-----NSLWKGSLSRCPSH 215
Db 214 VTFNLSIYLNIOQRTRFLDLGAREAGPEPPPEAQPSPPPPGCGWCKGHEAMPLH 273
Qy 216 -----AGFIATSSRGTHSRRTGLACTSLPGLKEPAASHSSSPRGKSLLV 263
Db 274 RYGVGEAAVGAEGEATLGGGGGGGS-----VASPTSSG-----SSSRGTERPR----- 318
Qy 264 SLRTHMSGSIAPKVGSCFCSSESPVTLHQ-----EHVELLRGKRLARSIAVLSSAF 314
Db 319 -----SLKRGSKPSSASSLEKRMKMSVQSFTQRFRLSRDRKVAKSLAVISIF 367

QY 137 VAVMILAFVNGPMILASDSWK-----NSTNTECEPGFVTEWYILAITAFLEFLPVSL 191
Db 161 LLVWVLAFLYGPAIL---SWEYLSGGSSIPGHCYAEFFYNWYFLITASTLEFFTPFLS 217
QY 192 VVYFSVQIY-----WSLWKRGSLSRCPSH 215
Db 218 VTFNLSIYLNQIRTRRLDGLDGAAREAGAPPPPEAQSPPPPGCGWCKGKGHEAMPLH 277
QY 216 -----AGFIATSSRGTHSRRTGLACRTSLPGLKEPAASLHSESPRGKSSLLV 263
Db 278 RYGVGEAAVGAAGEATLGGGGGGS-----VASPTSSG-----SSSRGTERPR 322
QY 264 SLRTHMSGSTIAFKVGSFCSESPVLHQR-----EHVELLRGKGLARSLAVLLSAF 314
Db 323 -----SLKRGSKPSASSASLEKRMKMWVSQSFTQRFRLSRDRKVAKSLAVISIF 371
QY 315 AICWAPYCLFTIVLSTVRRGERPKSIWYSIAFWLQFNLSLNPFLYPLCHRRFKAFWKI 374
Db 372 GLCWAPYTLMLIIRAC-HGHCVPDYWYETSFLLWANSANVPLVPLCHHSFRRAFTKL 430
QY 375 LCVTK---QPAPS 384
Db 431 LCPQKLIKIPHSS 443

RESULT 13

US-09-891-053-20
; Sequence 20, Application US/09891053
; Patent No. 6750322
; GENERAL INFORMATION:
; APPLICANT: Itadani, Hiraku
; APPLICANT: Takimura, Tetsuo
; APPLICANT: Nakamura, Takao
; APPLICANT: Kobayashi, Masahiko
; APPLICANT: Tanaka, Ken-ichi
; APPLICANT: Hidaka, Yusuke
; APPLICANT: Ohta, Masataka
; TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)
; FILE REFERENCE: 06501-083001
; CURRENT APPLICATION NUMBER: US/09/891, 053
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: PCT/JP99/07280
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: PCT/JP98/05967
; PRIOR FILING DATE: 1998-12-25
; PRIOR APPLICATION NUMBER: JP 11/145661
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-891-053-20

Query Match 33.9%; Score 693; DB 2; Length 453;
Best Local Similarity 37.6%; Pred. No. 1.6e-51;
Matches 163; Conservative 50; Mismatches 124; Indels 96; Gaps 11;
QY 18 LAPMLSLAPATIGNAVVILAFVADRNLRHSNYFFLNLAISDFPVGVISIPLYIPHTL 77
Db 37 LAALMALLIVATVGNALVMAFVADSSLRQTQNNFFLNLAISDFLVGAFICPLYVPYVL 96
QY 78 F-NWNPSSGICMFWLITDYLLCTASVYSLVSYDRYQSVSNVAVRAOHTGLKIVAO 136
Db 97 TGRWTFGRGLCKLWLVVDYLLCTSSAFNVLISYDRFLSVTRAVSYRAOQGDTRRAVR 156
QY 137 VAVMILAFVNGPMILASDSWK-----NSTNTECEPGFVTEWYILAITAFLEFLPVSL 191
Db 157 LLVWVLAFLYGPAIL---SWEYLSGGSSIPGHCYAEFFYNWYFLITASTLEFFTPFLS 213
QY 192 VVYFSVQIY-----WSLWKRGSLSRCPSH 215

Db 214 VTFNLSIYLNQIRTRRLDGLDGAAREAGAPPPPEAQSPPPPGCGWCKGKGHEAMPLH 273
QY 216 -----AGFIATSSRGTHSRRTGLACRTSLPGLKEPAASLHSESPRGKSSLLV 263
Db 274 RYGVGEAAVGAAGEATLGGGGGGS-----VASPTSSG-----SSSRGTERPR 318
QY 264 SLRTHMSGSTIAFKVGSFCSESPVLHQR-----EHVELLRGKGLARSLAVLLSAF 314
Db 319 -----SLKRGSKPSASSASLEKRMKMWVSQSFTQRFRLSRDRKVAKSLAVISIF 367
QY 315 AICWAPYCLFTIVLSTVRRGERPKSIWYSIAFWLQFNLSLNPFLYPLCHRRFKAFWKI 374
Db 368 GLCWAPYTLMLIIRAC-HGHCVPDYWYETSFLLWANSANVPLVPLCHHSFRRAFTKL 426
QY 375 LCVTK---QPAPS 384
Db 427 LCPQKLIKIPHSS 439

RESULT 14

US-09-891-053-1
; Sequence 1, Application US/09891053
; Patent No. 6750322
; GENERAL INFORMATION:
; APPLICANT: Itadani, Hiraku
; APPLICANT: Takimura, Tetsuo
; APPLICANT: Nakamura, Takao
; APPLICANT: Kobayashi, Masahiko
; APPLICANT: Tanaka, Ken-ichi
; APPLICANT: Hidaka, Yusuke
; APPLICANT: Ohta, Masataka
; TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)
; FILE REFERENCE: 06501-083001
; CURRENT APPLICATION NUMBER: US/09/891, 053
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: PCT/JP99/07280
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: PCT/JP98/05967
; PRIOR FILING DATE: 1998-12-25
; PRIOR APPLICATION NUMBER: JP 11/145661
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 413
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-891-053-1

Query Match 33.7%; Score 690; DB 2; Length 413;
Best Local Similarity 38.6%; Pred. No. 2.6e-51;
Matches 160; Conservative 48; Mismatches 121; Indels 86; Gaps 10;
QY 18 LAPMLSLAPATIGNAVVILAFVADRNLRHSNYFFLNLAISDFPVGVISIPLYIPHTL 77
Db 37 LAALMALLIVATVGNALVMAFVADSSLRQTQNNFFLNLAISDFLVGAFICPLYVPYVL 96
QY 78 F-NWNPSSGICMFWLITDYLLCTASVYSLVSYDRYQSVSNVAVRAOHTGLKIVAO 136
Db 97 TGRWTFGRGLCKLWLVVDYLLCASSVFNVLISYDRFLSVTRAVSYRAOQGDTRRAVR 156
QY 137 VAVMILAFVNGPMILASDSWK-----NSTNTECEPGFVTEWYILAITAFLEFLPVSL 191
Db 157 ALVWVLAFLYGPAIL---SWEYLSGGSSIPGHCYAEFFYNWYFLITASTLEFFTPFLS 213
QY 192 VVYFSVQIY-----WSLWKRGSLSRCPSH 215
Db 214 VTFNLSIYLNQIRTRRLDGLDGAAREAGAPPPPEAQSPPPPGCGWCKGKGHEAMPLH 273
QY 216 AGFIATSSRGTHSRRTGLACRTSLPGLKEPAASLHSESPRGKSSLLVSLRTHMSGSTIA 275

Db 274 SS--GSSSRGTERPR-----SLKRGSKPSASSASLEKRMKM-----VSQSI-- 312
QY 276 FKVGSCRSFVHQHREHVELLRGRKLARSALVLLSAFAICWAPYCLFTIVLSTYRRGE 335
Db 313 -----TQFRLSRDKKVKAKSLAIIIVISFGLCWAPYLLMIIRAAC-HGR 355
QY 336 RPKSIWYSIAFWLQWNSLINPPLYPCLCHRRRFQKAFWKILCVTK---QPAPSQTQ 387
Db 356 CIPDYWYETSWLLWANSVNPVLYPLCHYSFRFAFTKLLCPQKLKQVPHGSLEQ 410

RESULT 15

US-09-165-543-5
; Sequence 5, Application US/09165543
; Patent No. 6093545
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl and Sandra Glucksmann
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,543
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/042,780
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: MNI-032CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 445 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-165-543-5

Query Match 33.3%; Score 682; DB 2; Length 445;
Best Local Similarity 37.0%; Pred. No. 1.4e-50;
Matches 160; Conservative 51; Mismatches 133; Indels 88; Gaps 10;

QY 18 LAFMSLLAFATIGNAVILAFVADRNLRHSNYFFLMLAISDFVGVISIPLYIPHTL 77
Db 37 LAALMALLIVATVIGNALVMAFVADSLRTQNFLLNLAISDFLVGAFCIPLYVPYVL 96
QY 78 F-NWNPSSGICMPWLITDYLCTASYSIVLISYDRYQSVSNARYRAOHTGILKIVQM 136
Db 97 TGRWTEGRGLCKULWLVVDLLCASSVFNIVLSYDRFLSVTRAVSRAOQDTRRAVRKM 156
QY 137 VAVWILAFLVNGPMILASDSWK-----NSTNTECEPGFVTEWYIILAITAFLEFLPVSL 191
Db 157 ALWVLAFLLYGPAIL---SWEVLSGSSISPEGHCAEFYFNWYFLITASTLEFFTPFLS 213
QY 192 VTYFSVQIY-----WSLWKGSLSRCPSH 215
Db 214 VTFFNLISYILNIQRRTRLDDGREGAPBPPDAPQSPPPAPPCWCWPKGHGEAMPLH 273

QY 216 AGFIATSSRG-----GHSRRRTGLACRTSLPGLKEPAASLHSESPPKSSLLVSLRT 267
Db 274 RYGVGEAGPGVEAGEAALGGSGGGAASPTSSG-----SSRGTGTERPR----- 318
QY 268 HMSGIILAFKVGSCRSFVHQHREHVELLRGRKLARSALVLLSAFAICW 318
Db 319 -----SLKRGSKPSASSASLEKRMKMVSQSIQFRFLSRDKKVKAKSLAIIIVISFGLCW 371
QY 319 APYCLFTIVLSTYRRGERPKSIWYSIAFWLQWNSLINPPLYPCLCHRRRFQKAFWKILCVT 378
Db 372 APYTLMIIRAAC-HGRICIPDIWYETSWLLWANSVNPVLYPLCHYSFRFAFTKLLCPQ 430
QY 379 K---QPAPSQTQ 387
Db 431 KLVQVPHGSLEQ 442

Search completed: April 26, 2006, 20:47:41
Job time : 29 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 26, 2006, 20:57:34 ; Search time 163 Seconds
(without alignments)
1002.278 Million cell updates/sec

Title: US-10-626-126-9
Perfect score: 2045
Sequence: 1 MSESNGTDVLPVLAQVPLAF.....WKILCVTKQAPASQTSQSVSS 391

Scoring table: BLOSOM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/prodata/1/pubpa/US07_PUBCOMB.pap:
2: /cgn2_6/prodata/1/pubpa/US08_PUBCOMB.pap:
3: /cgn2_6/prodata/1/pubpa/US09_PUBCOMB.pap:
4: /cgn2_6/prodata/1/pubpa/US10A_PUBCOMB.pap:
5: /cgn2_6/prodata/1/pubpa/US10B_PUBCOMB.pap:
6: /cgn2_6/prodata/1/pubpa/US11_PUBCOMB.pap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2045	100.0	391	5	US-10-626-445-9
2	2045	100.0	391	5	US-10-626-126-9
3	2045	100.0	391	5	US-10-626-398-9
4	1735	84.8	391	5	US-10-626-445-8
5	1735	84.8	391	5	US-10-626-126-8
6	1735	84.8	391	5	US-10-626-398-8
7	1403.5	68.6	390	3	US-09-812-216-2
8	1403.5	68.6	390	3	US-09-910-411-2
9	1403.5	68.6	390	3	US-09-875-076-14
10	1403.5	68.6	390	3	US-09-876-252-14
11	1403.5	68.6	390	3	US-09-852-165-2
12	1403.5	68.6	390	3	US-09-891-138A-6
13	1403.5	68.6	390	4	US-10-052-193-2
14	1403.5	68.6	390	4	US-10-225-567A-629
15	1403.5	68.6	390	4	US-10-272-983-14
16	1403.5	68.6	390	4	US-10-354-769-2
17	1403.5	68.6	390	4	US-10-393-807-14
18	1403.5	68.6	390	4	US-10-417-820A-14
19	1403.5	68.6	390	4	US-10-349-253A-2
20	1403.5	68.6	390	4	US-10-696-673-2
21	1403.5	68.6	390	4	US-10-723-955-14
22	1403.5	68.6	390	4	US-10-782-596-14
23	1403.5	68.6	390	4	US-10-737-619-2
24	1403.5	68.6	390	5	US-10-626-445-2
25	1403.5	68.6	390	5	US-10-684-206-20
26	1403.5	68.6	390	5	US-10-616-088-2
27	1403.5	68.6	390	5	US-10-626-126-2

28	1403.5	68.6	390	5	US-10-626-398-2	Sequence 2, Appli
29	1403.5	68.6	390	5	US-10-756-149-4702	Sequence 4702, Ap
30	1403.5	68.6	390	5	US-10-723-955-14	Sequence 14, Appli
31	1403.5	68.6	390	5	US-10-488-421-8	Sequence 8, Appli
32	1398.5	68.4	390	4	US-10-290-078-27	Sequence 27, Appli
33	1398.5	68.4	390	5	US-10-488-421-6	Sequence 6, Appli
34	1236.5	60.5	389	5	US-10-626-445-10	Sequence 10, Appli
35	1236.5	60.5	389	5	US-10-626-126-10	Sequence 10, Appli
36	1236.5	60.5	389	5	US-10-626-398-10	Sequence 10, Appli
37	1233	60.3	357	5	US-10-488-421-4	Sequence 4, Appli
38	1117.5	54.6	336	5	US-10-488-421-2	Sequence 2, Appli
39	698	34.1	445	4	US-10-453-106-2	Sequence 2, Appli
40	698	34.1	445	5	US-10-735-963-2	Sequence 2, Appli
41	693	33.9	445	3	US-09-350-206-2	Sequence 2, Appli
42	693	33.9	445	3	US-09-349-755-2	Sequence 2, Appli
43	693	33.9	445	3	US-09-166-334-2	Sequence 2, Appli
44	693	33.9	445	4	US-10-282-958-2	Sequence 2, Appli
45	693	33.9	445	4	US-10-225-567A-549	Sequence 549, App

ALIGNMENTS

RESULT 1
US-10-626-445-9
; Sequence 9, Application US/10626445
; Publication No. US20040248252A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0032
; CURRENT APPLICATION NUMBER: US/10/626,445
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Rattus rattus
US-10-626-445-9

Query Match	100.0%	Score	2045	DB	5	Length	391
Best Local Similarity	100.0%	Pred. No.	1.2e-183				
Matches	391	Conservative	0	Mismatches	0	Indels	0
Gaps	0						
QY	1	MSESNGTDVLPVLAQVPLAFPLMSLLAFATIGNAVVILAFVADRNLRHRSNYFFLNLAIS	60				
Db	1	MSESNGTDVLPVLAQVPLAFPLMSLLAFATIGNAVVILAFVADRNLRHRSNYFFLNLAIS	60				
QY	61	DFPVGVISPLYPHTLFWNNPGSGICMFWLITDYLLCTASVYSIVLISYDRQSVSNV	120				
Db	61	DFPVGVISPLYPHTLFWNNPGSGICMFWLITDYLLCTASVYSIVLISYDRQSVSNV	120				
QY	121	RYRAQHTGILKIVAQNVAVVILAFVNGPMLASDSWKSTNTEECBPGFVTEWYILAIT	180				
Db	121	RYRAQHTGILKIVAQNVAVVILAFVNGPMLASDSWKSTNTEECBPGFVTEWYILAIT	180				
QY	181	AFLEFLLPVSVVYFVSQIYWSLWKRGSLSRCPSHAGFIATSRGTGHSRRTGLACRTSL	240				
Db	181	AFLEFLLPVSVVYFVSQIYWSLWKRGSLSRCPSHAGFIATSRGTGHSRRTGLACRTSL	240				
QY	241	PGLKEPAASLHSESPRGKSSLLVSLTHMSGSLIAFKVGSFCRSESFVLQREHVELLRG	300				
Db	241	PGLKEPAASLHSESPRGKSSLLVSLTHMSGSLIAFKVGSFCRSESFVLQREHVELLRG	300				
QY	301	RKLARSLAVLLSAFAICWAPYCLFTIVLSTYRGERPKSIWYSIAFWLQFNSLINPFLY	360				
Db	301	RKLARSLAVLLSAFAICWAPYCLFTIVLSTYRGERPKSIWYSIAFWLQFNSLINPFLY	360				

QY 361 PLCHRRFQAFWKILCVTKQAPAPOTSQSVSS 391
Db 361 PLCHRRFQAFWKILCVTKQAPAPOTSQSVSS 391

RESULT 2

US-10-626-126-9

; Sequence 9, Application US/10626126
; Publication No. US20050074770A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0033
; CURRENT APPLICATION NUMBER: US/10/626,126
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Rattus rattus
US-10-626-126-9

Query Match 100.0%; Score 2045; DB 5; Length 391;
Best Local Similarity 100.0%; Pred. No. 1.2e-183;
Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSESNGTDVLP LTAQVPLAFLMSLLAPAITIGNAVVILAFVADRNLRHRSNFFFLNLAIS 60
Db 1 MSESNGTDVLP LTAQVPLAFLMSLLAPAITIGNAVVILAFVADRNLRHRSNFFFLNLAIS 60
QY 61 DFFVGVISIP LYPHTLFNNPSSGICMPWLITDYLCTASVVISVILISYDRYQSVNAV 120
Db 61 DFFVGVISIP LYPHTLFNNPSSGICMPWLITDYLCTASVVISVILISYDRYQSVNAV 120
QY 121 RYRAQHTGILKIVAQMVAWVILAFVNGPMLASDSKNSNTTECEPGFVTEWYILAIT 180
Db 121 RYRAQHTGILKIVAQMVAWVILAFVNGPMLASDSKNSNTTECEPGFVTEWYILAIT 180
QY 181 AFLEFLLPVSLVVFVSVQIYWSLWKSGLSRCPSHAGFIATSSRGTHSRRTGLACRTSL 240
Db 181 AFLEFLLPVSLVVFVSVQIYWSLWKSGLSRCPSHAGFIATSSRGTHSRRTGLACRTSL 240
QY 241 PGLKEPAASLHSES PRGKSLVSLRTHMSGSI IAPKVGSCRSBPVLHQREHVLELLRG 300
Db 241 PGLKEPAASLHSES PRGKSLVSLRTHMSGSI IAPKVGSCRSBPVLHQREHVLELLRG 300
QY 301 RKLARSLAVLLSAFAICWAPYCLFTIVLSTYRRGERPKSIWYSIAFWLQWNSLINPFLY 360
Db 301 RKLARSLAVLLSAFAICWAPYCLFTIVLSTYRRGERPKSIWYSIAFWLQWNSLINPFLY 360
QY 361 PLCHRRFQAFWKILCVTKQAPAPOTSQSVSS 391
Db 361 PLCHRRFQAFWKILCVTKQAPAPOTSQSVSS 391

RESULT 3

US-10-626-398-9

; Sequence 9, Application US/10626398
; Publication No. US20050074841A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0034
; CURRENT APPLICATION NUMBER: US/10/626,398
; CURRENT FILING DATE: 2003-07-23

; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Rattus rattus
US-10-626-398-9

Query Match 100.0%; Score 2045; DB 5; Length 391;
Best Local Similarity 100.0%; Pred. No. 1.2e-183;
Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSESNGTDVLP LTAQVPLAFLMSLLAPAITIGNAVVILAFVADRNLRHRSNFFFLNLAIS 60
Db 1 MSESNGTDVLP LTAQVPLAFLMSLLAPAITIGNAVVILAFVADRNLRHRSNFFFLNLAIS 60
QY 61 DFFVGVISIP LYPHTLFNNPSSGICMPWLITDYLCTASVVISVILISYDRYQSVNAV 120
Db 61 DFFVGVISIP LYPHTLFNNPSSGICMPWLITDYLCTASVVISVILISYDRYQSVNAV 120
QY 121 RYRAQHTGILKIVAQMVAWVILAFVNGPMLASDSKNSNTTECEPGFVTEWYILAIT 180
Db 121 RYRAQHTGILKIVAQMVAWVILAFVNGPMLASDSKNSNTTECEPGFVTEWYILAIT 180
QY 181 AFLEFLLPVSLVVFVSVQIYWSLWKSGLSRCPSHAGFIATSSRGTHSRRTGLACRTSL 240
Db 181 AFLEFLLPVSLVVFVSVQIYWSLWKSGLSRCPSHAGFIATSSRGTHSRRTGLACRTSL 240
QY 241 PGLKEPAASLHSES PRGKSLVSLRTHMSGSI IAPKVGSCRSBPVLHQREHVLELLRG 300
Db 241 PGLKEPAASLHSES PRGKSLVSLRTHMSGSI IAPKVGSCRSBPVLHQREHVLELLRG 300
QY 301 RKLARSLAVLLSAFAICWAPYCLFTIVLSTYRRGERPKSIWYSIAFWLQWNSLINPFLY 360
Db 301 RKLARSLAVLLSAFAICWAPYCLFTIVLSTYRRGERPKSIWYSIAFWLQWNSLINPFLY 360
QY 361 PLCHRRFQAFWKILCVTKQAPAPOTSQSVSS 391
Db 361 PLCHRRFQAFWKILCVTKQAPAPOTSQSVSS 391

RESULT 4

US-10-626-445-8

; Sequence 8, Application US/10626445
; Publication No. US20040248252A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0032
; CURRENT APPLICATION NUMBER: US/10/626,445
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-626-445-8

Query Match 84.8%; Score 1735; DB 5; Length 391;
Best Local Similarity 84.7%; Pred. No. 1.7e-154;
Matches 331; Conservative 17; Mismatches 43; Indels 0; Gaps 0;

QY 1 MSESNGTDVLP LTAQVPLAFLMSLLAPAITIGNAVVILAFVADRNLRHRSNFFFLNLAIS 60

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Db      1 MSESNTGILPPAAQVPLAFLMSFAPAIMVGNVILAFVVDNRNLRHSNYFFLNLAIS 60
Qy      61 DFPVGVISPLYIPHTLFNNPGSGICMFWLITDYLLCTASVYIVLISYDRYQSVNAV 120
Db      61 DFLVGLISPLYIPHYLFNNFGSGICMFWLITDYLLCTASVYIVLISYDRYQSVNAV 120
Qy     121 RYRAQHTGILKIVAOQVAVVILAFVNGPMLASDSWKNSNTTECEPGFVTEWYILAIT 180
Db     121 SYRAQHTGIMKIVAOQVAVVILAFVNGPMLASDSWKNSNTTKDCEPGFVTEWYILAIT 180
Qy     181 AFLFELLPSLVVYFVSQIYWSLWKRGSLSRCPESHAGFIATSSRGTHGSHRRRTGLACTSL 240
Db     181 MLLEFLLPVSIVAYFNVQIYWSLWKRRLSRCPESHAGFTSSSSASGHLHRAGVACRTSN 240
Qy     241 PGLKEPAASLHSESPPRKSSILVSLRTHMSSGSIAPFKVGSFRCSESPVLHQRHVELLRG 300
Db     241 PGLKESAAASHSESPPRKSSILVSLRTHMSSITAFKVGSMFSESAALRQRYAEALLRG 300
Qy     301 RKLARSAILLSAFAICWAPYCLFTIVLSTYRRGERPKSIWYSIAFWLQWNSLINFPLY 360
Db     301 RKLARSAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWNSFVNPFPLY 360
Qy     361 PLCHRRFQKAFWKILCVTKOPAPSQTQSVSS 391
Db     361 PLCHRRFQKAFWKILCVTKWPALSONQSVSS 391
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RESULT 5

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US-10-626-126-8
; Sequence 8, Application US/10626126
; Publication No. US20050074770A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0033
; CURRENT APPLICATION NUMBER: US/10/626,126
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-626-126-8
```

```
Query Match      84.8%; Score 1735; DB 5; Length 391;
Best Local Similarity 84.7%; Pred. No. 1.7e-154;
Matches 331; Conservative 17; Mismatches 43; Indels 0; Gaps 0;

Qy      1 MSESNTDVLPLTAQVPLAFLMSLAFATIGNAVILAFVADNRNLRHSNYFFLNLAIS 60
Db      1 MSESNTGILPPAAQVPLAFLMSFAPAIMVGNVILAFVVDNRNLRHSNYFFLNLAIS 60
Qy     61 DFPVGVISPLYIPHTLFNNPGSGICMFWLITDYLLCTASVYIVLISYDRYQSVNAV 120
Db     61 DFLVGLISPLYIPHYLFNNFGSGICMFWLITDYLLCTASVYIVLISYDRYQSVNAV 120
Qy     121 RYRAQHTGILKIVAOQVAVVILAFVNGPMLASDSWKNSNTTECEPGFVTEWYILAIT 180
Db     121 SYRAQHTGIMKIVAOQVAVVILAFVNGPMLASDSWKNSNTTKDCEPGFVTEWYILAIT 180
Qy     181 AFLFELLPSLVVYFVSQIYWSLWKRGSLSRCPESHAGFIATSSRGTHGSHRRRTGLACTSL 240
Db     181 MLLEFLLPVSIVAYFNVQIYWSLWKRRLSRCPESHAGFTSSSSASGHLHRAGVACRTSN 240
Qy     241 PGLKEPAASLHSESPPRKSSILVSLRTHMSSGSIAPFKVGSFRCSESPVLHQRHVELLRG 300
Db     241 PGLKESAAASHSESPPRKSSILVSLRTHMSSITAFKVGSMFSESPVLHQRHVELLRG 300
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Db     241 PGLKESAAASHSESPPRKSSILVSLRTHMSSITAFKVGSMFSESAALRQRYAEALLRG 300
Qy     301 RKLARSAILLSAFAICWAPYCLFTIVLSTYRRGERPKSIWYSIAFWLQWNSLINFPLY 360
Db     301 RKLARSAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWNSFVNPFPLY 360
Qy     361 PLCHRRFQKAFWKILCVTKOPAPSQTQSVSS 391
Db     361 PLCHRRFQKAFWKILCVTKWPALSONQSVSS 391
```

RESULT 6

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US-10-626-398-8
; Sequence 8, Application US/10626398
; Publication No. US20050074841A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0034
; CURRENT APPLICATION NUMBER: US/10/626,398
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-626-398-8
```

```
Query Match      84.8%; Score 1735; DB 5; Length 391;
Best Local Similarity 84.7%; Pred. No. 1.7e-154;
Matches 331; Conservative 17; Mismatches 43; Indels 0; Gaps 0;

Qy      1 MSESNTDVLPLTAQVPLAFLMSLAFATIGNAVILAFVADNRNLRHSNYFFLNLAIS 60
Db      1 MSESNTGILPPAAQVPLAFLMSFAPAIMVGNVILAFVVDNRNLRHSNYFFLNLAIS 60
Qy     61 DFPVGVISPLYIPHTLFNNPGSGICMFWLITDYLLCTASVYIVLISYDRYQSVNAV 120
Db     61 DFLVGLISPLYIPHYLFNNFGSGICMFWLITDYLLCTASVYIVLISYDRYQSVNAV 120
Qy     121 RYRAQHTGILKIVAOQVAVVILAFVNGPMLASDSWKNSNTTECEPGFVTEWYILAIT 180
Db     121 SYRAQHTGIMKIVAOQVAVVILAFVNGPMLASDSWKNSNTTKDCEPGFVTEWYILAIT 180
Qy     181 AFLFELLPSLVVYFVSQIYWSLWKRGSLSRCPESHAGFIATSSRGTHGSHRRRTGLACTSL 240
Db     181 MLLEFLLPVSIVAYFNVQIYWSLWKRRLSRCPESHAGFTSSSSASGHLHRAGVACRTSN 240
Qy     241 PGLKEPAASLHSESPPRKSSILVSLRTHMSSGSIAPFKVGSFRCSESPVLHQRHVELLRG 300
Db     241 PGLKESAAASHSESPPRKSSILVSLRTHMSSITAFKVGSMFSESAALRQRYAEALLRG 300
Qy     301 RKLARSAILLSAFAICWAPYCLFTIVLSTYRRGERPKSIWYSIAFWLQWNSLINFPLY 360
Db     301 RKLARSAILLSAFAICWAPYCLFTIVLSTYPRTERPKSVWYSIAFWLQWNSFVNPFPLY 360
Qy     361 PLCHRRFQKAFWKILCVTKOPAPSQTQSVSS 391
Db     361 PLCHRRFQKAFWKILCVTKWPALSONQSVSS 391
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RESULT 7

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US-09-812-216-2
; Sequence 2, Application US/09812216
; Publication No. US20020098539A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Jiang Xu
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[illegible]

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; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,131
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/141,448
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/156,653
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,633
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,555
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,634
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/157,280
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,294
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,281
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,293
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,282
; PRIOR FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-875-076-14

Query Match      68.6%; Score 1403.5; DB 3; Length 390;
Best Local Similarity 69.1%; Pred. No. 2.8e-123;
Matches 271; Conservative 78; Mismatches 78; Indels 3; Gaps 2;

QY      1  MSESNGTDLPLTAQVPLATLMSLAFATIGNAVVLAFVADRNLRHRSNYFFLNLAIS 60
DB      1  MPTNSTINLSLSTRVTLAFPMSLVAFAMIGNALVILAFVVDKLRHRSYFFLNLAIS 60

QY      61  DFFVGVISIPLYPHITLFFNNPSCGICMFWLITDYLCTASVYSIVLISYDRYQSVNAV 120
DB      61  DFFVGVISIPLYPHITLFEWDFGKEICVFWLTIDYLCTASVYVNLVILSYDRYLSVNAV 120

QY      121  RYRAQHTGILKIVAOVAVWILAFVNGPMLASDSWKNSTNTECEPGFVFWYILAIT 180
DB      121  SYRTQHTGVLIKIVTAVVAVWVLAFLVNGPMLVSVESWKDEGS--ECEPGFSEWYILAIT 178

QY      181  AFLEFLLPVLVYVFSQIYVSLWKRGSLRCPSHAGFIATSSRGTCGHSRRTGLACRTSL 240
DB      179  SFLEFVIPVTLVAYFNNNIYVSLWKRDHLRCSQSHPLGTAVSSNICGHSFGRLSRRSL 238

QY      241  PGLKEPAASLHRSRPGKSSLLVSLRTHMSGSIIAFKVGSFCSRSESPVLHQREHVELLRG 300
DB      239  SASTEPASFSRQRKSSLMFSSTTKMNSNTIASKGSFQSDSVLHQREHVELLRA 298

QY      301  RKLARSLAVLSAFAICWAPYCLFTVILSTRGERPKSIWYIAFWLQFNLSLNPFLY 360
DB      299  RRLAKSLAILLGVFAVCWAPYSLFTVILSVSSATGPKSVWYIRIAFWLQFNFSVNPFLY 358

QY      361  PLCHRPQKAFKWLICVTQKOPAPSO--TQSVSS 391
DB      359  PLCHGRFQKAFKIFCIKKQPLFSQHSRSVSS 390

RESULT 10
US-09-876-252-14
; Sequence 14, Application US/09876252
; Publication No. US20030018182A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Lowitz, Kevin P.
```

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; APPLICANT: Lin, I-Lin
; APPLICANT: Dang, Huong T.
; APPLICANT: Chen, Kuoping
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: Non-Endogenous Constitively Activated Human G Protein Coupled Rec
; FILE REFERENCE: AREN-0054
; CURRENT APPLICATION NUMBER: US/09/876,252
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 09/416,760
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/110,060
; PRIOR FILING DATE: 1998-11-27
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,852
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/123,944
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,945
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,948
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,951
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/152,524
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/151,114
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/108,029
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,127
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,131
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/141,448
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/156,555
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,634
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,653
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/157,280
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,294
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,281
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,282
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/156,633
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
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Qy 361 PLCHRRFQKAPFKILCVTKQAPSQ-TQSVSS 391
Db 359 PLCHRRFQKAPFKILCVTKQAPSQ-TQSVSS 390

RESULT 13

US-10-052-193-2

; Sequence 2, Application US/10052193

; Publication No. US20020132755A1

; GENERAL INFORMATION:

; APPLICANT: Pfizer, Inc.

; TITLE OF INVENTION: HISTAMINE RECEPTOR ANTAGONISTS

; FILE REFERENCE: PC10963A

; CURRENT APPLICATION NUMBER: US/10/052,193

; CURRENT FILING DATE: 2002-01-17

; PRIOR FILING DATE: 2001-01-17

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2

; LENGTH: 390

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-052-193-2

Query Match 68.6%; Score 1403.5; DB 4; Length 390;

Best Local Similarity 69.1%; Pred. No. 2.8e-123;

Matches 271; Conservative 40; Mismatches 78; Indels 3; Gaps 2;

Qy 1 MSESNGTDVPLTAQVPLAFPLMSLLAFPAITIGNAVVILAFVADRNLRHRSNYFPLNLAI 60

Db 1 MPDNTNINLSLSTRVTLAFPMFLVAFALMGNALVILAFVDDKLRHRSNYFPLNLAI 60

Qy 61 DFFVGVISIPLYIPIHTLFNWNPGSGICMFMLITDYLCTASVSVILISYDRYQSVSNV 120

Db 61 DFFVGVISIPLYIPIHTLFNWNPGSGICMFMLITDYLCTASVSVILISYDRYQSVSNV 120

Qy 121 RYRAQHTGILKIVAQVAVWILAFPLVNGPMILASDWSKNTNTECEPGFVTEWYILAIT 180

Db 121 SYRTOHTGVLKIVTLMAVAVWILAFPLVNGPMILVSESWKDEGS--ECEPGFSEWYILAIT 178

Qy 181 AFLEFLLPVSLVYVPSQIYVLSLWKRGSLSRCPSHAGFIATSRGTGHSRRTGLACTSL 240

Db 179 SFLEFVPIVLVAFYNNIYVLSLWKRDLHRCQHPGLTAVSSNICHSFRGLSSRRSL 238

Qy 241 PGLKEPAASLHSESPRGKSSLLVSLRTHMSGIIFAFKVGSCFCSSESPVLHQREHVELLRG 300

Db 239 SASTEVPAFHSERQRRKSSLMFSSRTKMSNTIASKMGFSQSDSVALLHQREHVELLRA 298

Qy 301 RKLARSALLSAPAIQWAPYCLFTIVLSYRRGERPKSIWYSIAFWLQWNSLINPFLY 360

Db 299 RRLAKSAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLNFSFVNPLLY 358

Qy 361 PLCHRRFQKAPFKILCVTKQAPSQ-TQSVSS 391

Db 359 PLCHRRFQKAPFKILCVTKQAPSQ-TQSVSS 390

RESULT 14

US-10-225-567A-629

; Sequence 629, Application US/10225567A

; Publication No. US20030113798A1

; GENERAL INFORMATION:

; APPLICANT: LifeSpan Biosciences

; APPLICANT: Brown, Joseph P.

; APPLICANT: Burmer, Glenn C.

; APPLICANT: Roush, Christine L.

; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS

; FILE REFERENCE: 1920-4-4

; CURRENT APPLICATION NUMBER: US/10/225,567A

; CURRENT FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: 60/2257,144

; PRIOR FILING DATE: 2000-12-19

; NUMBER OF SEQ ID NOS: 2292

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 629

; LENGTH: 390

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-225-567A-629

Query Match 68.6%; Score 1403.5; DB 4; Length 390;

Best Local Similarity 69.1%; Pred. No. 2.8e-123;

Matches 271; Conservative 40; Mismatches 78; Indels 3; Gaps 2;

Qy 1 MSESNGTDVPLTAQVPLAFPLMSLLAFPAITIGNAVVILAFVADRNLRHRSNYFPLNLAI 60

Db 1 MPDNTNINLSLSTRVTLAFPMFLVAFALMGNALVILAFVDDKLRHRSNYFPLNLAI 60

Qy 61 DFFVGVISIPLYIPIHTLFNWNPGSGICMFMLITDYLCTASVSVILISYDRYQSVSNV 120

Db 61 DFFVGVISIPLYIPIHTLFNWNPGSGICMFMLITDYLCTASVSVILISYDRYQSVSNV 120

Qy 121 RYRAQHTGILKIVAQVAVWILAFPLVNGPMILASDWSKNTNTECEPGFVTEWYILAIT 180

Db 121 SYRTOHTGVLKIVTLMAVAVWILAFPLVNGPMILVSESWKDEGS--ECEPGFSEWYILAIT 178

Qy 181 AFLEFLLPVSLVYVPSQIYVLSLWKRGSLSRCPSHAGFIATSRGTGHSRRTGLACTSL 240

Db 179 SFLEFVPIVLVAFYNNIYVLSLWKRDLHRCQHPGLTAVSSNICHSFRGLSSRRSL 238

Qy 241 PGLKEPAASLHSESPRGKSSLLVSLRTHMSGIIFAFKVGSCFCSSESPVLHQREHVELLRG 300

Db 239 SASTEVPAFHSERQRRKSSLMFSSRTKMSNTIASKMGFSQSDSVALLHQREHVELLRA 298

Qy 301 RKLARSALLSAPAIQWAPYCLFTIVLSYRRGERPKSIWYSIAFWLQWNSLINPFLY 360

Db 299 RRLAKSAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLNFSFVNPLLY 358

Qy 361 PLCHRRFQKAPFKILCVTKQAPSQ-TQSVSS 391

Db 359 PLCHRRFQKAPFKILCVTKQAPSQ-TQSVSS 390

RESULT 15

US-10-272-983-14

; Sequence 14, Application US/10272983

; Publication No. US20030148450A1

; GENERAL INFORMATION:

; APPLICANT: Chen, Ruoping

; APPLICANT: Dang, Huong T.

; APPLICANT: Liaw, Chen W.

; APPLICANT: Lin, I-Lin

; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors

; FILE REFERENCE: AREN0050

; CURRENT APPLICATION NUMBER: US/10/272,983

; CURRENT FILING DATE: 2002-10-17

; PRIOR APPLICATION NUMBER: US/09/417,044

; PRIOR FILING DATE: 1999-10-12

; PRIOR APPLICATION NUMBER: 60/109,213

; PRIOR FILING DATE: 1998-11-20

; PRIOR APPLICATION NUMBER: 60/120,416

; PRIOR FILING DATE: 1999-02-16

; PRIOR APPLICATION NUMBER: 60/121,851

; PRIOR FILING DATE: 1999-02-26

; PRIOR APPLICATION NUMBER: 60/123,946

; PRIOR FILING DATE: 1999-03-12

; PRIOR APPLICATION NUMBER: 60/123,949

; PRIOR FILING DATE: 1999-03-12

; PRIOR APPLICATION NUMBER: 60/136,436

; PRIOR FILING DATE: 1999-05-28

; PRIOR APPLICATION NUMBER: 60/136,437

; PRIOR FILING DATE: 1999-05-28

; PRIOR APPLICATION NUMBER: 60/136,439

; PRIOR FILING DATE: 1999-05-28

; PRIOR APPLICATION NUMBER: 60/136,567


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; PRIOR FILING DATE: 1999-05-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-272-983-14

Query Match      58.6%; Score 1403.5; DB 4; Length 390;
Best Local Similarity 69.1%; Pred. No. 2.8e-123;
Matches 271; Conservative 40; Mismatches 78; Indels 3; Gaps 2;

Qy 1 MSESNGTDVLPPLTAQVPLAFLMSILLAPAITIGNAVTILAFVADRNLRHRSNYFFLNLAIS 60
Db 1 MPDINSTINLSLSTRVTLPFLMFLVPAFALMGALVILAFVVDKNLRHRSYFFLNLAIS 60

Qy 61 DFFVGVISIPLYIPHTLFWNNPGSGICMFWLIITDYLLCTASVYSIVLISYDRYOSVSNV 120
Db 61 DFFVGVISIPLYIPHTLFEWDFGKEICVFWLTDTLLCTASVYNIVLISYDRYLSVSNV 120

Qy 121 RYRAQHTGILKIIVAOVAVVILAFVLNPGMILASDSWKNSTNTERCEPGFVTEWYILAIT 180
Db 121 SYRTOHTGVLLKIVTLMVAVVWLAFVLNPGMILVSESWKDEGS--ECEPGFSEWYILAIT 178

Qy 181 AFLEFLLPVSLVVVFSVQIYWSLWKGSLSCPCSHAGFIATSSRGTGCHSRRTGLACRTSL 240
Db 179 SFLEFVLPVLVAYFNNIYWSLWKRDLHSLRCQSHPGLTAVSSNICGHSPGRLSRRSL 238

Qy 241 PGLKEPAASLHSESPRGKSLVSLRTHMSGSIIFKVGSCFCSSESPVLHQREHVELLRG 300
Db 239 SASTEVPASTHSEQRKKSLSMFSSRTKMNSNTIASKMGFSQSDSVALHQREHVELLRA 298

Qy 301 RKLARSLAVLLSAPACWAPCYCLFTIVLSTYRRGERPKSIWYSIAFWLQWFNSLNPFLY 360
Db 299 RRLAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLFQWFNSFVNPLLY 358

Qy 361 PLCHRRFQKAFWKILCVTKOPAPSQ-TQSVSS 391
Db 359 PLCHKRQKAFLLKIFCIKKQPLFSQHSRVSS 390
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Search completed: April 26, 2006, 21:01:11
Job time : 165 secs

QY 264 SLRTHMSGSIIAFKVGSFCRSESPVLHOR-----EHVELLRGRKLARSIAVLISAF 314
Db 319 -----SLKRGSKPASASLASLEKRMKWSQSFTQRFRLSRDRKVKASLAVISIF 367
QY 315 AICWAPYCLFTIVLSTYRGERPKSIWYSIAFLQWNSLINPFLYPLCHRRRQKAFWKI 374
Db 368 GLCWAPYTLMLIIRAAC-HGHCVPDYWYETSFLLWANSVAVNPVLYPLCHHSFRRAFTKL 426
QY 375 LCVTK-----QPAPSOQTQ 387
Db 427 LCPQKLIQPHSSLEQ 442
RESULT 2
US-11-115-564-1
; Sequence 1, Application US/11115564
; Publication No. US20050267116A1
; GENERAL INFORMATION:
; APPLICANT: Peschke, Bernd
; APPLICANT: Hohlweg, Rolf
; TITLE OF INVENTION: SUBSTITUTED HEXAHYDROPYRROLO[1,2-A]PYRAZINES,
; TITLE OF INVENTION: OCTAHYDROPYRIDO[1,2-A]PYRAZINES AND
; TITLE OF INVENTION: DECAHYDROPYRAZINO[1,2-A]AZEPINES
; FILE REFERENCE: 6483.200-US
; CURRENT APPLICATION NUMBER: US/11/115,564
; CURRENT FILING DATE: 2005-04-27
; PRIOR APPLICATION NUMBER: US 60/387,047
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: Danish Application no. PA 2002 00863
; PRIOR FILING DATE: 2002-06-06
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-115-564-1
Query Match 33.9%; Score 693; DB 7; Length 445;
Best Local Similarity 37.6%; Pred. No. 1.3e-53;
Matches 163; Conservative 50; Mismatches 124; Indels 96; Gaps 11;
QY 18 LAFMLSLAFAITIGNAVVILAFVADNRLRHSNYFPLNLAIISDFPVGVISIPLYIPHTL 77
Db 37 LAALMALLIVATVIGNALVMLAFVADSSLRTONFFLLNLAIISDFLVGAFICFLYIPYVL 96
QY 78 F-WNPNPGSGICMFLLITDYLLCTASVYSIVLSIDRYQSVNAVRYRAQHTGILKIVAQM 136
Db 97 TGRWTFGRGLCKLWLVVDYLLCTSSAFNIVLSIDRYFSLVTRAVSYRAQQDTRRAVRKM 156
QY 137 VAWVILAFVNGPMILASDSWK-----NSTNTECECPGFVTEWYILAITAFLEFLPVSL 191
Db 157 LLVWVLAFLLYGPAIL---SWEYLSGGSSIPGHCYAEFFYNWYFLITASTLEFFTPFLS 213
QY 192 VVYFSVOIY-----NSLWKRGSLSRCPSH 215
Db 214 VTFPNLSIYLNIOQRTRLRLDGAAREAGPPEPPAQPSPPPPCWCWGKHGEAMPLH 273
QY 216 -----AGFIATSSRGTHSRRTGLACRTSLPGLKEPAASLHSESPPRGKSSLLV 263
Db 274 RYGVGEAAVGAEGEATLGGGGGGS-----VASFTSSG-----SSSRGTERPR----- 318
QY 264 SLRTHMSGSIIAFKVGSFCRSESPVLHOR-----EHVELLRGRKLARSIAVLISAF 314
Db 319 -----SLKRGSKPASASLASLEKRMKWSQSFTQRFRLSRDRKVKASLAVISIF 367
QY 315 AICWAPYCLFTIVLSTYRGERPKSIWYSIAFLQWNSLINPFLYPLCHRRRQKAFWKI 374
Db 368 GLCWAPYTLMLIIRAAC-HGHCVPDYWYETSFLLWANSVAVNPVLYPLCHHSFRRAFTKL 426
QY 375 LCVTK-----QPAPSOQTQ 384

Db 427 LCPQKLIQPHSS 439
RESULT 3
US-11-115-564-3
; Sequence 3, Application US/11115564
; Publication No. US20050267116A1
; GENERAL INFORMATION:
; APPLICANT: Peschke, Bernd
; APPLICANT: Hohlweg, Rolf
; TITLE OF INVENTION: SUBSTITUTED HEXAHYDROPYRROLO[1,2-A]PYRAZINES,
; TITLE OF INVENTION: OCTAHYDROPYRIDO[1,2-A]PYRAZINES AND
; TITLE OF INVENTION: DECAHYDROPYRAZINO[1,2-A]AZEPINES
; FILE REFERENCE: 6483.200-US
; CURRENT APPLICATION NUMBER: US/11/115,564
; CURRENT FILING DATE: 2005-04-27
; PRIOR APPLICATION NUMBER: US 60/387,047
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: Danish Application no. PA 2002 00863
; PRIOR FILING DATE: 2002-06-06
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Rat
US-11-115-564-3
Query Match 33.3%; Score 682; DB 7; Length 445;
Best Local Similarity 37.0%; Pred. No. 1.2e-52;
Matches 160; Conservative 51; Mismatches 133; Indels 88; Gaps 10;
QY 18 LAFMLSLAFAITIGNAVVILAFVADNRLRHSNYFPLNLAIISDFPVGVISIPLYIPHTL 77
Db 37 LAALMALLIVATVIGNALVMLAFVADSSLRTONFFLLNLAIISDFLVGAFICFLYIPYVL 96
QY 78 F-WNPNPGSGICMFLLITDYLLCTASVYSIVLSIDRYQSVNAVRYRAQHTGILKIVAQM 136
Db 97 TGRWTFGRGLCKLWLVVDYLLCASSVFNIVLSIDRYFSLVTRAVSYRAQQDTRRAVRKM 156
QY 137 VAWVILAFVNGPMILASDSWK-----NSTNTECECPGFVTEWYILAITAFLEFLPVSL 191
Db 157 ALVWVLAFLLYGPAIL---SWEYLSGGSSIPGHCYAEFFYNWYFLITASTLEFFTPFLS 213
QY 192 VVYFSVOIY-----NSLWKRGSLSRCPSH 215
Db 214 VTFPNLSIYLNIOQRTRLRLDGAAREAGPPEPPAQPSPPPPCWCWGKHGEAMPLH 273
QY 216 AGFIATSSRGTHSRRTGLACRTSLPGLKEPAASLHSESPPRGKSSLLVSLRT 267
Db 274 RYGVGEAGPQVEAGEAALGGSGGGAASPTSSSG-----SSSRGTERPR----- 318
QY 268 HMSGSIIAFKVGSFCRSESPVLHOR-----EHVELLRGRKLARSIAVLISAFICW 318
Db 319 -----SLKRGSKPASASLASLEKRMKWSQSFTQRFRLSRDRKVKASLAVISIFGLCW 371
QY 319 APYCLFTIVLSTYRGERPKSIWYSIAFLQWNSLINPFLYPLCHRRRQKAFWKILCVT 378
Db 372 APYTLMLIIRAAC-HGRCIPDYWYETSFLLWANSVAVNPVLYPLCHHSFRRAFTKLCPQ 430
QY 379 K---QPAPSOQTQ 387
Db 431 KLKVQPHGSLEQ 442

RESULT 4
US-11-241-956-3
; Sequence 3, Application US/11241956
; Publication No. US20060024792A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS INC.; BAUGHN, Mariah R.;
; APPLICANT: GRAUL Richard C.; CHAWLA, Narinder K.;
; APPLICANT: GANDHI, Ameena R.; HAPALIA, April J.A.;

```
; APPLICANT: RAMKUMAR, Javalaxmi; TRIBOUTEV, Catherine M.;
; APPLICANT: THORNTON, Michael B.; KALLICK, Deborah A.;
; APPLICANT: YAO, Monique G.; ELLIOTT, Vicki S.;
; APPLICANT: BURFORD, Neil; KHAN, Farrah A.;
; APPLICANT: YUE, Henry; LU, Yan;
; APPLICANT: ARVIZU, Chandra S.; ROOPA, Reddy M.;
; APPLICANT: NGUYEN, Daniel B.; LEE, Ernestine A.;
; APPLICANT: LU, Dzung Aina M.; ISON, Craig H.;
; APPLICANT: WALSH, Roderick T.; POLICKY, Jennifer L.
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: PI-0236 USN
; CURRENT APPLICATION NUMBER: US/11/241,956
; CURRENT FILING DATE: 2005-10-04
; PRIOR APPLICATION NUMBER: US/10/398,036
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: PCT/US01/30661
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/245,855
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/242,322
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 60/240,589
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US 60/249,343
; PRIOR FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: US 60/247,587
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/245,900
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/242,223
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 60/236,546
; PRIOR FILING DATE: 2000-09-29
; SOFTWARE: PERL Program
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 3
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7474823CD1
US-11-241-956-3

Query Match      29.0%; Score 594; DB 7; Length 441;
Best Local Similarity 67.3%; Pred. No. 7.3e-45;
Matches 115; Conservative 17; Mismatches 29; Indels 10; Gaps 3;

QY 47 RHRSNYFFLN----LAISDFP-----VGVISIPLYIPHTLFWNPGSGICMFMLITDYLLC 98
Db 92 RERTNLVLMKKWFEVLPDPTFEVTQQSVISIPLYIPHTLFEWDFGKEICVFMLITDYLLC 151
QY 99 TASVYSIVLSYDRYQSVSNVAVRAQHTGILKIVAOVAVIILAFVNGPMLIASWSK 158
Db 152 TASVYNIVLSYDRYLSVSNVAVRYRTQTVGLKIVTLVAVVIAFLVNGPMLIVSESK 211
QY 159 NSTNTECEPGFTWETYLITAFLEPLLVSVLVVYFVSQVYWSLMKRGSL 209
Db 212 DEGS--ECEPGFTSEWYILAITSFLEFVPIPVILVAYFNMMIYWSLMKRDHL 260

RESULT 5
US-11-124-368A-183
; Sequence 183, Application US/11124368A
; Publication No. US20050287559A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: James J. Devlin
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof
; FILE REFERENCE: CU001524
; CURRENT APPLICATION NUMBER: US/11/124,368A

; APPLICANT: RAMKUMAR, Javalaxmi; TRIBOUTEV, Catherine M.;
; APPLICANT: THORNTON, Michael B.; KALLICK, Deborah A.;
; APPLICANT: YAO, Monique G.; ELLIOTT, Vicki S.;
; APPLICANT: BURFORD, Neil; KHAN, Farrah A.;
; APPLICANT: YUE, Henry; LU, Yan;
; APPLICANT: ARVIZU, Chandra S.; ROOPA, Reddy M.;
; APPLICANT: NGUYEN, Daniel B.; LEE, Ernestine A.;
; APPLICANT: LU, Dzung Aina M.; ISON, Craig H.;
; APPLICANT: WALSH, Roderick T.; POLICKY, Jennifer L.
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: PI-0236 USN
; CURRENT APPLICATION NUMBER: US/11/241,956
; CURRENT FILING DATE: 2005-10-04
; PRIOR APPLICATION NUMBER: US/10/398,036
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: PCT/US01/30661
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/245,855
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/242,322
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 60/240,589
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US 60/249,343
; PRIOR FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: US 60/247,587
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/245,900
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/242,223
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 60/236,546
; PRIOR FILING DATE: 2000-09-29
; SOFTWARE: PERL Program
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 3
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7474823CD1
US-11-241-956-3

Query Match      19.7%; Score 403.5; DB 7; Length 590;
Best Local Similarity 24.3%; Pred. No. 7.1e-28;
Matches 131; Conservative 85; Mismatches 163; Indels 161; Gaps 19;

QY 2 SESNGTDVLPPLTAQ-----VPLAFMLSLAFATIGNAVVILAFVADRLNLRHSNYPFLN 56
Db 50 SSPDGTDDPLGGHTVQVVFIAFLTGILAVTIIGNILVIVSPKYNKQLKTVNNYFLLS 109
QY 57 LAISDFPVGVISIPLYIPHTLFWNPGSGICMFMLITDYLLCTASVYSIVLSYDRYQSV 115
Db 110 LACADLIIGVISMNLFTTYIMRWALGNLACDLWLDAIDYVASNASVMNLLVISDFRYS 169
QY 116 VSNVAVRYAQTGILKIVAOVAV--WILAFVNGPMLIASDSW-----KNSTNTECEPG 169
Db 170 ITRPLTYRAKRT--TKRAGVMIGLAWVIFVLWAPAIL---FWQYFVGKRTVPFGECFIQ 224
QY 170 FVTEWILAITAFLEPLLVSVLVVYFVSQVYWSLMKRG-----SLPG----- 242
Db 225 FLESEPTITGTATAAAYMPVTINTI-----LYWRIYKETEKTKELAGLQASGTEAETENF 280
QY 207 ----GSLSRCPs-----HAGF----- 218
Db 281 VHPGTSSRSCSSYELQQSMKRSNRKRGCRHFWFTTKSWKPSSEQMDQDSSSDSWNNN 340
QY 219 -IATSRGTGHSRRTGLACRT-----SLPG----- 242
Db 341 DAAASLENSASDEEDIGSETRAIYSIVLKLPGHSTILNSTKLPSDDNLQVPEELGMVD 400
QY 243 LKEPAASLHSES-----PRCKSSLLVSLR-----THMSGSI-----IAPKV 278
Db 401 LERKADKLAQKSVDDGGSPKSPKLPQLQESAVDTAKTSDVNSVSGKSTALPLSFKE 460
QY 279 GS----FCHSESPVLHOREHVELLRGRKLARSIAVLLSAFAICWAPYCLFTVILSTYRRG 334
Db 461 ATLAKEFALKTRSQITKRKRMSLVKEKAAQTLAAILAFIITWTPVYIMVLV-NTFCDS 519
QY 335 ERPKSITWYSIAFWLQWNSLINPFLYPLCHRRPQKAPFKIL----CVTKQAPSPQTSQSVSS 391
Db 520 CIPKFTW-NLGYWLCYINSTVNPVYALCNKTRFTTFFKMLLLCCQCKKRRKKQYQOQRS 578

RESULT 6
US-11-127-877-54
; Sequence 54, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; TITLE OF INVENTION: Amyloid-Beta Protein Production
; FILE REFERENCE: P27, 800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/503,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
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; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 41
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-127-877-41

Query Match      17.7%; Score 361; DB 7; Length 466;
Best Local Similarity 24.5%; Pred.No.3.le-24;
Matches 115; Conservative 85; Mismatches 157; Indels 112; Gaps 17;

QY   2 SEANGTDVLP LTAQ-----VPLAFMLSLAFAITIGNAVVILAFADNRNLHRHSNYFFL 55
DB   |:::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY   56 NLAISDPFVGVISIPLYPIHTLFN--MNPFGSGICMFWLITDYLLCTASVYSIVLSIDRYQ 114
DB   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY   64 SLACADLIIGVFSNNLYTLTVIGYPLGVPVCDLWLDALDVVSNASVMNLLIISFDRYF 123
DB   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY   115 SVNAVRYRAQTGILKIVAQMV-AVWILAFLVNGPMILASDSWK-----NSTWTBCEP 168
DB   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY   124 CVTKPLTYPVKR--TKMGAGMTAAAWLVLSFILMAPAIL---FWQFTVGVRTVEDGECY 178
DB   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY   169 GFTEWVILAITAFLEPLLPSVLVVVFESVOIYNSLWKGSLSR-----CP 213
DB   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY   179 QFFSNAAVTGTAIAAPLYPLIMTV----LYWHI-SRASKRIKKDKKEPVANQDVPSP 233
DB   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY   214 S-----HAGFIATSSRGTHSR--RTGLACR-----237
DB   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY   234 SLVQGRIVKPNNMPSSDDGLEHNKIQNGKAPRDPTVENCVQEKESSNDSTSVA 293
DB   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY   238 -----TSL-----PGLUKEPAASHSESPRGKSLVLVSLRTHMSG-----272
DB   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY   294 SNMRDDEITODENTVSTSLGHSDKENSQTCIRIGTKPKSDSCPTNTTVEVVGSSGQN 353
DB   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY   273 -----LIAFKVGSFCSESPLHQREHVELLGRKLARSLAVLSAFAICWAPYCLFTI 326
DB   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY   354 GDEKQNVARKIVKMTQKA-----KKPPPSREKKVTTRILAILLAFIITWAPYNM-V 407
DB   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY   327 VLSTYRRGERPKSIWYSIAFWLQFNLSINPFYPLCHRRFQKAFWKIL 375
DB   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY   408 LIWFCACTPNVTW-TIGWLCYINSTINPACYALCNATFKTKTKHL 455
DB   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

RESULT 10
US-11-127-877-51
; Sequence 51. Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: Amyloid-Beta Protein Production
; CURRENT APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 51
; LENGTH: 429
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-127-877-51

Query Match      17.5%; Score 357.5; DB 7; Length 429;
Best Local Similarity 25.5%; Pred.No.5.8e-24;
Matches 106; Conservative 77; Mismatches 142; Indels 91; Gaps 20;
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Db 134 SITQAIENLKRTP-RRKAIITVVVISAVISFPPLISIEKKGSGGQPOAEP RCEIND 192
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Search completed: April 26, 2006, 21:01:43
Job time : 27 secs

GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 29, 2006, 01:31:43 ; Search time 249 Seconds
(without alignments)
2791.272 Million cell updates/sec

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Perfect score: 2045
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Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Database : Issued Patents NA:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1403.5	68.6	1173	3	US-09-414-010-1
2	1403.5	68.6	1173	3	US-09-812-216-1
3	1403.5	68.6	1173	3	US-09-875-076-13
4	693	33.9	1335	2	US-08-985-090-3
5	693	33.9	1335	3	US-09-165-543-3
6	693	33.9	1335	3	US-09-167-354-6
7	693	33.9	1335	3	US-09-642-855-6
8	693	33.9	1335	3	US-09-642-514-6
9	693	33.9	1335	3	US-09-642-852-6

10	693	33.9	2050	3	US-09-891-053-21	Sequence 21, Appl
11	693	33.9	2665	3	US-09-949-016-5059	Sequence 5059, Ap
12	693	33.9	2689	2	US-08-985-090-1	Sequence 1, Appli
13	693	33.9	2689	3	US-09-165-543-1	Sequence 5, Appli
14	693	33.9	2699	3	US-09-167-354-5	Sequence 5, Appli
15	693	33.9	2699	3	US-09-642-855-5	Sequence 5, Appli
16	693	33.9	2699	3	US-09-642-514-5	Sequence 5, Appli
17	693	33.9	2699	3	US-09-642-852-5	Sequence 5, Appli
18	690	33.7	1239	3	US-09-891-053-2	Sequence 5, Appli
19	690	33.7	2700	3	US-09-891-053-5	Sequence 5, Appli
20	682	33.3	1338	3	US-09-165-543-6	Sequence 26, Appli
21	682	33.3	1953	3	US-09-891-053-26	Sequence 4, Appli
22	617	30.2	3244	3	US-09-165-543-4	Sequence 1, Appli
23	617	30.2	1056	3	US-09-524-162-1	Sequence 6, Appli
24	538	26.3	1086	2	US-08-985-090-6	Sequence 33, Appli
25	538	26.3	1086	3	US-09-165-543-33	Sequence 4, Appli
26	538	26.3	2218	2	US-08-985-090-4	Sequence 31, Appli
27	538	26.3	2218	3	US-09-165-543-31	Sequence 1314, Ap
28	405	19.8	1913	3	US-09-016-434-1314	Sequence 6, Appli
29	401	19.6	1956	2	US-08-313-553-6	Sequence 6, Appli
30	401	19.6	1956	3	US-08-767-393-6	Sequence 176, App
31	400.5	19.6	1233	3	US-09-721-870-176	Sequence 516, App
32	400	19.6	1773	3	US-09-826-509-516	Sequence 1176, Ap
33	400	19.6	2261	3	US-09-016-434-1176	Sequence 1411, Ap
34	395.5	19.3	1742	3	US-09-016-434-1411	Sequence 520, App
35	395	19.3	1599	3	US-09-826-509-520	Sequence 158, App
36	393.5	19.2	4008	3	US-09-976-594-158	Sequence 3, Appli
37	388.5	19.0	1386	2	US-09-016-434-1339	Sequence 3, Appli
38	387.5	18.9	1690	3	US-08-461-812-3	Sequence 3, Appli
39	387.5	18.9	1690	3	US-09-371-705-3	Sequence 1258, Ap
40	387.5	18.9	2635	3	US-09-016-434-1258	Sequence 426, App
41	386.5	18.9	1173	3	US-09-826-509-426	Sequence 512, App
42	382.5	18.7	1422	3	US-09-826-509-512	Sequence 8, Appli
43	379.5	18.6	1581	2	US-08-313-553-8	Sequence 8, Appli
44	379.5	18.6	1581	3	US-08-767-393-8	Sequence 13, Appl
45	377.5	18.5	1893	3	US-09-891-053-13	

ALIGNMENTS

RESULT 1
US-09-414-010-1
; Sequence 1, Application US/09414010
; Patent No. 6204017
; GENERAL INFORMATION:
; APPLICANT: Behan, Jiang Xu
; APPLICANT: Hedrick, Joseph A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Monsema, Frederick J. Jr.
; APPLICANT: Morse, Kelley L.
; APPLICANT: Umland, Shelby P.
; APPLICANT: Wang, Suke
; TITLE OF INVENTION: Histamine receptor
; FILE REFERENCE: CN01069
; CURRENT APPLICATION NUMBER: US/09/414,010
; CURRENT FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-414-010-1

Alignment Scores:
Pred. No.: 1.5e-133 Length: 1173
Score: 1403.50 Matches: 271
Percent Similarity: 79.3% Conservative: 40
Best Local Similarity: 69.1% Mismatches: 78
Query Match: 68.6% Indels: 3
DB: 3 Gaps: 2
US-10-626-126-9 (1-391) x US-09-414-010-1 (1-1173)

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; Sequence 1, Application US/09812216
; Patent No. 6613533
; GENERAL INFORMATION:
; APPLICANT: Behan, Jiang Xu
; APPLICANT: Hedrick, Joseph A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Monsma, Frederick J. Jr.
; APPLICANT: Morse, Kelley L.
; APPLICANT: Umland, Shelby P.
; APPLICANT: Wang, Suke
; TITLE OF INVENTION: Histamine receptor
; FILE REFERENCE: CN01069
; CURRENT APPLICATION NUMBER: US/09/812,216
; CURRENT FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 09/414,010
; PRIOR FILING DATE: 1999-10-07
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-812-216-1
Alignment Scores:
Pred. No.: 1-5e-133 Length: 1173
Score: 1403.50 Matches: 271
Percent Similarity: 79.3% Conservative: 40
Best Local Similarity: 69.1% Mismatches: 78
Query Match: 68.6% Indels: 3
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US-10-626-126-9 (1-391) x US-09-812-216-1 (1-1173)
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Db 1075 CCATTTGTGTCAACAGCGCTTCAAAAGCGTTCTTGAATAATTTGTATAAAAAAGCAA 1134
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RESULT 3

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US-09-875-076-13
; Sequence 13, Application US/09875076
; Patent No. 6869776
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCES: AREN0050
; CURRENT APPLICATION NUMBER: US/09/875,076
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
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; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,127
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,131
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/141,448
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/156,653
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,633
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,555
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,634
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/157,280
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,294
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,281
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,293
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,282
; PRIOR FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-875-076-13

Alignment Scores:
Pred. No.: 1,5e-133 Length: 1173
Score: 1403.50 Matches: 271
Percent Similarity: 79.3% Conservative: 40
Best Local Similarity: 69.1% Mismatches: 78
Query Match: 68.6% Indels: 3
DB: Gaps: 2

US-10-626-126-9 (1-391) x US-09-875-076-13 (1-1173)
Qy 1 MetSerGluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe 20
Db 1 ATGCCAGATACTAATAGCAACAATCAATTTATCACTAAGCACTCGTGTACTTTAGCATTT 60
Qy 21 LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValVallIleLeuAlaPhe 40
Db 61 TTTATGCTCTTAGTAGCTTTTGTATAATGCTAGGAAATGCTTTGGTCAATTTAGCTTTT 120
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Qy 81 AsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100
Db 241 GATTTTGGAAAGGAAATCTGTGATTTTGGCTCACTACTGACTATCTGTGTATGTACAGCA 300
Qy 101 SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
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Db 301 TCTGTATATAACATGTGCTCATCAGCTATGATCGATACCTGTCAGTCTCAAAATGCTGTG 360
Qy 121 ArgTyrArgAlaGlnHisThrGlyIleLeuValIleValAlaGlnMetValAlaValTtp 140
Db 361 TCTTATAGAACTCAACATCTGGGCTCTGAAGATTGTACTCTGATGGTGGCGGTTGG 420
Qy 141 IleLeuAlaPheLeuValAenGlyProMetIleLeuAlaSerAspSerTrpIlysAenSer 160
Db 421 GTGCTGGCTTCTTAGTGAATGGCCCAATGATTTCTAGTTTCAGAGTCTTGGAGGATGAA 480
Qy 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTrpTyrIleLeuAlaIleThr 180
Db 481 GGTAGT-----CAATGTGAACCTGGATTTTTTTCGAATGGTACATCTCTTGCATCACA 534
Qy 181 AlaPheLeuGluPheLeuProValSerLeuValValTyrPheSerValGlnIleTyr 200
Db 535 TCATTTTGGAAATTCGTGATCCAGTCATCTTAGTCGTTATTTCAACATGAATATTAT 594
Qy 201 TrpSerLeuTrpIysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220
Db 595 TGGAGCTGTGGAGGTGATCATCTCAGTAGTGGCCAAAGCCATCTCTGGACTGACTGCT 654
Qy 221 ThrSerSerArgGlyThrGlyHisSerArgThrGlyLeuAlaCysArgThrSerLeu 240
Db 655 GTCTCTTCCAACATCTGTGGACACTCATTCAAGAGTAGACTATCTTCAAGGAGATCTCT 714
Qy 241 ProGlyLeuGluProAlaAlaSerLeuHisSerGluSerProArgGlyIysSerSer 260
Db 715 TCTGCATCGACAAGTTCCTGCATCTCTTCATTCAGAGAGACAGAGGAGAAAGTAGT 774
Qy 261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleAlaPheIysValGlySer 280
Db 775 CTATGTTTCTTCAAGAACCAAGATGAATAGCAATCAATGCTTCCAAATGGGTTC 834
Qy 281 PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300
Db 835 TTCTCCAAATCAGATCTGTAGCTCTTCAAAAGGGAACATGTTGAACTGCTTAGAGCC 894
Qy 301 ArgIysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
Db 895 AGGAGATTAGCCAAGTCACTGGGCCATCTCTTAGGGGTTTTCGTGTTGCTGGGCTCCA 954
Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProIysSerIle 340
Db 955 TATCTCTGTTCAAATGTCCTTCAATTTATTCCTCAGCAACAGTCTCAATCAGTT 1014
Qy 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAenPropheLeuTyr 360
Db 1015 TGGTATAGAATTGCAATTTGGCTTCAGTGGTTCAATTCCTTTGTCAATCTCTTTGTAT 1074
Qy 361 ProLeuCysHisArgArgPheGlnIysAlaPheTrpIysIleLeuCysValThrIysGln 380
Db 1075 CCATTGTGCACAGCGCTTCAAAAGGCTTCTTGAATAATATTGTATATAAAAGCAA 1134
Qy 381 ProAlaProSerGln---ThrGlnSerValSerSer 391
Db 1135 CCTCTACCATCACACACAGTCGGTCAGTATCTTCT 1170
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RESULT 4

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US-08-985-090-3
; Sequence 3, Application US/08985090
; Patent No. 5885893
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl
; TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
```

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,090
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jean M. Silveri
; REGISTRATION NUMBER: 39,030
; REFERENCE/DOCKET NUMBER: MNI-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1335 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1335
; US-08-985-090-3
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Alignment Scores:
Pred. No.: 8,2e-61 Length: 1335
Score: 693.00 Matches: 163
Percent Similarity: 49.2% Conservative: 50
Best Local Similarity: 37.6% Mismatches: 124
Query Match: 33.9% Indels: 96
DB: 2 Gaps: 11
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US-10-626-126-9 (1-391) x US-08-985-090-3 (1-1335)

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Qy 18 LeuAlaPheLeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValAlaIle 37
Db 109 CTGGCGCGCTCATGGCGTGTCTCATCGTGGCGCACGCTGTGGCAACGCTGTGGTCATG 168
Qy 38 LeuAlaPheValAlaAspArgAenLeuArgHisArgSerAsnTyrPhePheLeuAenLeu 57
Db 169 CTCGCCCTTCGTGGCGGACTCGAGCCTCCGACCCAGAACAACTTCTCTGCTCAACCTC 228
Qy 58 AlaIleSerAspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeu 77
Db 229 GCCATCTCCGACTTCTCTCGCGGCGCTTCTGCATCCCACTGTATGTCACCTACGTGCTG 288
Qy 78 Phe---AsnTrpAsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeu 96
Db 289 ACAGCGCGCTGGACCTTCGCGCGGGGCTCTGCAAGCTGTGGCTGTAGTGGACTACCTG 348
Qy 97 LeuCysThrAlaSerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerVal 116
Db 349 CTGTGCACCTCTCTCTGCTTCAACATGCTGCTCATCAGCTACGACCGCTTCTGTGGTC 408
Qy 117 SerAsnAlaValArgTyrArgAlaGlnHisThrGlyIleLeuIysIleValAlaGlnMet 136
Db 409 ACCCGAGCGGTCTCATACCGGCGCCAGAGGGGTGACACGCGGGGGGAGTCCGGAAGATG 468
Qy 137 ValAlaValTrpIleLeuAlaPheLeuValAenGlyProMetIleLeuAlaSerAspSer 156
Db 469 CTGCTGGTGTGGTGTCTGCGCTTCTCTGCTGTACGGACCAAGCCATCCTG-----AGC 519
Qy 157 TrpLys-----AsnSerThrAsnThrGluGluCysGluProGlyPheVal 171
Db 520 TGGAGTACCTGTTCGGGGGCGAGCTCCATCCCGAGGGCAGCTGCTATGCCGAGTCTTC 579
Qy 172 ThrGluTrpTyrIleLeuAlaIleThrAlaPheLeuGluPheLeuLeuProValSerLeu 191
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Db 580 TAACTGGTACTTCTCATACGGCTTCCACCGCTGAGTTCTTTACGCCCTTCTCAGC 639
Qy 192 ValValTyrPheSerValGlnIleTyr- 200
Db 640 GTACACTTCTTAACTCAGCATCTACTGAACATCCAGAGGCGCACCGCGCTCGGCTG 699
Qy 200 ----- 200
Db 700 GATGGGGCTCAGAGGCGAGCGCGCCGAGCCCTCCGAGGCGCCAGCTCACCACCC 759
Qy 201 -----TtpSerLeuTyrPheSerValGlnIleTyr- 215
Db 760 CCACCGCTGCTGCTGCGGCTGCTGCGAGAGGCGCACGGGAGGCGCATGCCCTGCAC 819
Qy 216 -----AlaGlyPheIleAlaThrSerSer 223
Db 820 AGTATGGGTGGGTGAGGCGCGTAGGCGCTGAGGCGCGGAGGCGGACCTCGGGGGT 879
Qy 224 ArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeuProGlyLeu 243
Db 880 GCGGTGGGGCGGCTCC-----GTGGCTTCCACCCACCTCCAGCTCCGGC--- 924
Qy 244 LysGluProAlaAlaSerGlnSerProArgGlyLysSerSerLeuVal 263
Db 925 -----AGCTCTCGAGGCGGCTGAGAGGCGCGC----- 954
Qy 264 SerLeuArgThrHisMetSerGlySerIleAlaPheLysValGlySerPheCysArg 283
Db 955 -----TCACCTCAGAGGGGCTCCAGCCCTCG 981
Qy 284 SerGluSerProValLeuHisGlnArg-----GluHis 294
Db 982 GCGTCTCGGCTCCTCATCTGAGAGGCGCATGAAGATGGTGTCCAGAGCTTCCACCGCGC 1041
Qy 295 ValGluLeuLeuArgGlyArgLysLeuAlaArgSerLeuAlaValLeuSerAlaPhe 314
Db 1042 TTTGGGCTGTCTCGGACAGAAAGTGGCTGCTGCGCGGTCATCGTGAGCATCTTT 1101
Qy 315 AlaIleCysTrpAlaProTyrCysLeuPheThrIleValLeuSerThrTyrArgArgGly 334
Db 1102 GGGCTGTGCTGGGCGCCCATACACCTGCTGATGATCATCGGCGCGCTGC---CATGGC 1158
Qy 335 GluArgProLysSerIleTyrPheSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeu 354
Db 1159 CACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1218
Qy 355 IleAsnProPheLeuTyrProLeuCysHisArgArgPheGlnLysAlaPheTrpLysVal 374
Db 1219 GTCAACCTGTGCTTCTACCTCTGTGCGCACACAGCTTCCGCGCGGCTTCCACCAAGCTG 1278
Qy 375 LeuCysValThrLys-----GlnProAlaProSer 384
Db 1279 CTCTGCCCCAGAGCTCAAAATCCAGCCCCACAGCTCC 1317
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RESULT 5

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US-09-165-543-3
; Sequence 3, Application US/09165543
; Patent No. 6093545
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl and Sandra Glucksman
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,543
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/042,780
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: MNI-032CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1335 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1335
; US-09-165-543-3
Alignment Scores:
Pred. No.: 8-2e-61 Length: 1335
Score: 693.00 Matches: 163
Percent Similarity: 49.2% Conservative: 50
Best Local Similarity: 37.6% Mismatches: 124
Query Match: 33.9% Indels: 96
DB: 3 Gaps: 11
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US-10-626-126-9 (1-391) x US-09-165-543-3 (1-1335)

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Qy 18 LeuAlaPheLeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValValle 37
Db 109 CTGGCGCGCTCATGGCGTCTCATGTGCCACGGTCTGGGCAACGGCTGTCATG 168
Qy 38 LeuAlaPheValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeu 57
Db 169 CTGGCGCTTGTGGCGGACTCGAGCCTCCGACCCAGAACCACTTCTTCTGCTCAACCTC 228
Qy 58 AlaIleSerAspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeu 77
Db 229 GCATCTCCGACTCTCTGCTGCGGCGCTTCTGATCCCACTATGTATGATACCTAGCTGCTG 288
Qy 78 Phe---AsnTrpAsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeu 96
Db 289 ACAGGCGCTGGACCTTCGGCGCGGGGCTCTGCAAGCTGTGGCTGTAGTGAGCTACCTG 348
Qy 97 LeuCysThrAlaSerValTyrSerIleValIleSerTyrAspArgTyrGlnSerVal 116
Db 349 CTGTGCACCTCTCTGCTTCAACATGCTGCTCATCAGCTACGACCGCTTCTCTGCTCGGTC 408
Qy 117 SerAsnAlaValArgTyrArgAlaGlnHisThrGlyIleLeuLysIleValAlaGlnMet 136
Db 409 ACCGAGCGGTCTCATACCGGCGCCAGCAGGTGACACGGCGGGGAGTGGCGAAGATG 468
Qy 137 ValAlaValTrpIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSer 156
Db 469 CTGCTGTGTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 519
Qy 157 TrpLys-----AsnSerThrAsnThrGluGluCysGluProGlyPheVal 171
Db 520 TGGAGTACCTGTCTCGGGGCGAGCTCCATCCCGAGGCGCCACTGCTATGCGAGTTCTTC 579
Qy 172 ThrGluTrpTyrIleLeuAlaIleThrAlaPheLeuGluPheLeuLeuProValSerLeu 191
Db 580 TACAACCTGGTACTTCTCTCATCAGGCTTCCACCGCTGGAGTTCTTTACGCCCTTCTCCTCAGC 639
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QY 192 ValValTyrPheSerValGlnIleTyr----- 200
DB 640 GTCACTTCTTTAACTCAGCATCTACCTGAACATCCAGAGGCGCACCCCGCTCCGGCTG 699

QY 200 ----- 200
DB 700 GATGGGGCTCGAGAGGCGAGCCGCCCGAGCCCTCCCGAGGCCCGCCCTCACCACCC 759
QY 201 -----TrpSerLeuTyrPheLysArgGlySerLeuSerArgCysProSerHis 215
DB 760 CCACCGCTGGCTGCTGGGCTCTGCGAGAGGGGCGACGGGAGGCCATGCGCGCTGCAC 819

QY 216 -----AlaGlyPheIleAlaThrSerSer 223
DB 820 AGTATGGGGTGGGTAGGCGCGCGCTAGGGCTGAGGCCCGGGAGGGGACCCCTCGGGGT 879
QY 224 ArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeuProGlyLeu 243
DB 880 GCGGGTGGGGCGGCTCC-----GTGGCTTACCCACCTCCAGCTCCGGC--- 924
QY 244 LysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSerLeuLeuVal 263
DB 925 -----AGCTCTCGAGGGGCACTGAGAGGCGCGC----- 954
QY 264 SerLeuArgThrHisMetSerGlySerIleIleAlaPheLysValGlySerPheCysArg 283
DB 955 -----TCACTCAAGAGGGGCTCCAAAGCGCTCG 981
QY 284 SerGluSerProValLeuHisGlnArg-----GluHis 294
DB 982 GCGTCTCGGCCCTCACTGGAGAGCGCATGAAGATGGTGCCAGAGCTTCACCCAGCGC 1041
QY 295 ValGluLeuLeuArgGlyArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPhe 314
DB 1042 TTTGGGTGTCTCGGGACAGAAAGTGGCCAGTGGCTGGCCGCTCATCGTGAACATCTT 1101
QY 315 AlaIleCysTrpAlaProTyrCysLeuPheThrIleValLeuSerThrTyrArgArgGly 334
DB 1102 GGGCTCTGTGGGCCCCATACAGCTGCTGATGATCATCCGGGCGCGCTGC---CATGGC 1158
QY 335 GluArgProLysSerIleTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeu 354
DB 1159 CACTGGCTCCCTGACTACTGTAGAAACCTCTCTGGCTCTGTGGGCGCAACTCGGCT 1218
QY 355 IleAsnProPheLeuTyrProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIle 374
DB 1219 GTCAACCGCTGCTCTACCTCTGTGCGCACACACAGCTTCCGCGGGGCTTCACCAAGCTG 1278

QY 375 LeuCysValThrLys-----GlnProAlaProSer 384
DB 1279 CTCTGCCCCAGAGCTCAAAATCCAGGCCCCACAGCTCC 1317
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RESULT 6

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US-09-167-354-6
; Sequence 6' Application US/09167354A
; Patent No. 6138559
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; FILE REFERENCE: SUBTYPE
; CURRENT APPLICATION NUMBER: US/09/167,354A
; CURRENT FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Artificial Sequence
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/ FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:CDNA
US-09-167-354-6
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Alignment Scores:
Pred. No.: 8.2e-61 Length: 1335
Score: 693.00 Matches: 163
Percent Similarity: 49.2% Conservative: 50
Best Local Similarity: 37.6% Mismatches: 124
Query Match: 33.9% Indels: 96
DB: 3 Gaps: 11
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US-10-626-126-9 (1-391) x US-09-167-354-6 (1-1335)

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QY 18 LeuAlaPheLeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValValIle 37
DB 109 CTGGCCGCGCTCATGGCGCTGCTCATCTGCGGCACCGTGTGGCAACGGCTGGTCATG 168
QY 38 LeuAlaPheValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeu 57
DB 169 CTGGCTTCTGGCGGCACTCGAGCTCCGACCCAGAACAACTTCTTCTGCTCAACCTC 228
QY 58 AlaIleSerAspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeu 77
DB 229 GCCATCTCGGACTTCTCTGCTGGCGCTTCTGTCATCCCATGTATGTACCTACGTGCTG 288
QY 78 Phe---AsnTrpAsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeu 96
DB 289 ACAGGCGCTGAGCTTCGGCGCGGCTCTGCAAGCTGTGGCTGTGTAGTGAGTACCTG 348
QY 97 LeuCysThrAlaSerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerVal 116
DB 349 CTGTGCACCTCTCTGCTTCAACATCGTGTCTCATCAGCTACGACCGCTTCTGTCGCTC 408
QY 117 SerAsnAlaValArgTyrArgAlaGlnHisThrGlyIleLeuLysIleValAlaGlnMet 136
DB 409 ACCCGAGCGGTCTCATACCGGGCCACAGAGGGTGACACGCGGGCGGCGAGTGCAGNAATG 468
QY 137 ValAlaValTrpIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSer 156
DB 469 CTGCTGTGGGTGTGGCTTCTGCTGTACGACCAAGCCATCCTG-----AGC 519
QY 157 TrpLys-----AsnSerThrAsnThrGluGluCysGluProGlyPheVal 171
DB 520 TGGGACTACTGTCCGGGGCGAGCTCATCCCGAGGGCGCACTGTATGCGAGTCTTCTTC 579
QY 172 ThrGluTrpTyrIleLeuAlaIleThrAlaPheLeuGluPheLeuProValSerLeu 191
DB 580 TACAACCTGGTACTTCTCATACGGCTTCCACCGCTGGAGTCTTTACGCGCTTCTCTCAGC 639
QY 192 ValValTyrPheSerValGlnIleTyr----- 200
DB 640 GTCACTTCTTTAACTCAGCATCTACCTGAACATCCAGAGGCGCACCCCGCTCCGGCTG 699
QY 200 ----- 200
DB 700 GATGGGGCTCGAGAGGCGAGCCGCCCGAGCCCTCCCGAGGCCCGCCCTCACCACCC 759
QY 201 -----TrpSerLeuTyrPheLysArgGlySerLeuSerArgCysProSerHis 215
DB 760 CCACCGCTGGCTGCTGGGCTCTGCGAGAGGGGCGACGGGAGGCCATGCGCGCTGCAC 819
QY 216 -----AlaGlyPheIleAlaThrSerSer 223
DB 820 AGTATGGGGTGGGTAGGCGCGCGCTAGGGCTGAGGCCCGGGAGGGGACCCCTCGGGGT 879
QY 224 ArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeuProGlyLeu 243
DB 880 GCGGGTGGGGCGGCTCC-----GTGGCTTACCCACCTCCAGCTCCGGC--- 924
QY 244 LysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSerLeuLeuVal 263
DB 925 -----AGCTCTCGAGGGGCACTGAGAGGCGCGC----- 954
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Qy 264 SerLeuArgThrHisMetSerGlySerIleAlaPheLysValGlySerPheCysArg 283
Db 955 :::::TCACCAAGAGGGGCTCCAAGCCGTCG 981
Qy 284 SerGluSerProValLeuHisGlnArg-----GluHis 294
Db 982 CGCTCCTCGGCTCGCTGGAGAGCGCATGAGATGGTGTCCAGAGCTTCACCCAGCGC 1041
Qy 295 ValGluLeuLeuArgGlyArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPhe 314
Db 1042 TTTCCGGCTGTCTCGGACAGGAAAGTGCCAAAGTCGCTCGCTCATCGTAGCATCTTT 1101
Qy 315 AlaIleCysTrpAlaProTyrCysLeuPheThrIleValLeuSerThrTyrArgArgGly 334
Db 1102 GGCTCTGTGGGCCCCATACAGCTGTGATGATCATCCGGGCGCGCTGC---CATGGC 1158
Qy 335 GluArgProLysSerIleTrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeu 354
Db 1159 CACTGGCTCCCTGACTACTGGTAGCAAACTCTCTTCTGGCTCTGTGGGCCAACTCGGCT 1218
Qy 355 IleAsnProPheLeuTyrProLeuCysHisArgPheGlnLysAlaPheTrpLysIle 374
Db 1219 GTCAACCTGTCTCTACCTCTGTGTCACACAGCTTTCGCGGGCTTTCACCAAGCTG 1278
Qy 375 LeuCysValThrLys-----GlnProAlaProSer 384
Db 1279 CTCTGCCCCAGAGCTCAAAATCCAGCCCCACAGCTCC 1317
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RESULT 7

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US-09-642-855-6
; Sequence 6, Application US/09642855
; Patent No. 6413743
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; FILE REFERENCE: JMW
; SUBTYPE
; CURRENT APPLICATION NUMBER: US/09/642,855
; PRIOR FILING DATE: 2000-08-21
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDNA
US-09-642-855-6
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Alignment Scores:
Pred. No.: 8.2e-61 Length: 1335
Score: 693.00 Matches: 163
Percent Similarity: 49.2% Conservative: 50
Best Local Similarity: 37.6% Mismatches: 124
Query Match: 33.9% Indels: 96
DB: 3 Gaps: 11
```

US-10-626-126-9 (1-391) x US-09-642-855-6 (1-1335)

```
Qy 18 LeuAlaPheLeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValIle 37
Db 109 CTGGCCCGCTCATGGCGCTGCTCATCGTGCCACGCTGTGGGCAACGCGTGTGTCATG 168
Qy 38 LeuAlaPheValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeu 57
Db 169 CTGCGCTCTGTGGCCGAGCTCGAGGCTCCGCCACCAAGAACTTCTTCTCTGCTCAACCTC 228
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Qy 58 AlaIleSerAspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeu 77
Db 229 GCCATCTCCGACTCTCTCGTTCGGCGCTTCTGCATCCACTGATGATACCTACCTAGCTGCTG 288
Qy 78 Phe---AsnTrpAsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeu 96
Db 289 ACAGGCGCTGGACCTTCGGCGGGGCTCTGCAAGCTGTGGCTGTAGTAGGACTACCTG 348
Qy 97 LeuCysThrAlaSerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerVal 116
Db 349 CTGTGACACTCTCTCTCCCTTCAACATCGTGTCTCATCAGCTACACCGCTTCTGTGCGGTC 408
Qy 117 SerAsnAlaValArgTyrArgAlaGlnHisThrGlyIleLeuLysIleValAlaGlnMet 136
Db 409 ACCGAGCGGTCTCATACCGGGCCAGAGGGTGACACGGCGGGGCGGAGTGCAGGAAGATG 468
Qy 137 ValAlaValTrpIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSer 156
Db 469 CTGCTGTGTGGTGTGGCTTCTCTGCTGTACGGACCGACCATCTCTG-----AGC 519
Qy 157 TrpLys-----AsnSerThrAsnThrGluGluCysGluProGlyPheVal 171
Db 520 TGGGAGTACCTGTTCGGGGGCGAGCTCCATCCCGAGGGCCACTGCTATGCGGAGTTCTTC 579
Qy 172 ThrGluTrpTyrIleLeuAlaIleThrAlaPheLeuGluPheLeuProValSerLeu 191
Db 580 TACAACCTGTGTACTCTCTCATCAGGGTTCACCCCTGGAGTCTTTAGCCCTTCTCTCAGC 639
Qy 192 ValValTyrPheSerValGlnIleTyr----- 200
Db 640 GTCACTCTCTTTAACTCAGCATCTACCTGAACATCCAGAGGGCGCACCCGCTCCGGCTG 699
Qy 200 ----- 200
Db 700 GATGGGGCTCGAGAGGCGAGCCGCCCGAGCCCTCCCGAGGCCAGCCCTCACCAACC 759
Qy 201 -----TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHis 215
Db 760 CCACCGCTGGTGTCTGGGGCTCTGTGAGAGGAGCGACGGGAGGCGCATGCGCTGCAC 819
Qy 216 -----AlaGlyPheIleAlaThrSerSer 223
Db 820 AGGTATGGGGTGGGTGAGGGCGCGTAGGCGCTGAGGCGCGGGAGCGGACCTCCGGGGT 879
Qy 224 ArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeuProGlyLeu 243
Db 880 GCGGTGGGGGCGGCTCC-----GTGGCTTCAACCACCTCCAGCTCCGCTCGGC--- 924
Qy 244 LysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSerLeuVal 263
Db 925 -----AGTCTCTGAGGGGCACTGAGAGGCGCGGC----- 954
Qy 264 SerLeuArgThrHisMetSerGlySerIleIleAlaPheLysValGlySerPheCysArg 283
Db 955 -----TCACTCAAGAGGGGCTCCAAGCCGTCG 981
Qy 284 SerGluSerProValLeuHisGlnArg-----GluHis 294
Db 982 CGCTCCTCGGCTCGCTGGAGAGCGCATGAGATGGTGTCCAGAGCTTTCACCCAGCGC 1041
Qy 295 ValGluLeuLeuArgGlyArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPhe 314
Db 1042 TTTCCGGCTGTCTCGGACAGGAAAGTGCGCTGTGGCTGTGGCTGTGGGCAACTCGGCT 1101
Qy 315 AlaIleCysTrpAlaProTyrCysLeuPheThrIleValLeuSerThrTyrArgArgGly 334
Db 1102 GGCTCTGTGGGCCCCATACAGCTGTGATGATCATCCGGGCGCGCTGC---CATGGC 1158
Qy 335 GluArgProLysSerIleTrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeu 354
Db 1159 CACTGGCTCCCTGACTACTGGTAGCAAACTCTCTTCTGGCTCTGTGGGCGCAACTCGGCT 1218
Qy 355 IleAsnProPheLeuTyrProLeuCysHisArgPheGlnLysAlaPheTrpLysIle 374
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; PRIOR FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDNA
US-09-642-852-6

Alignment Scores:
Pred. No.:      8.2e-61      Length:      1335
Score:          693.00      Matches:      163
Percent Similarity: 49.2%      Conservative: 50
Best Local Similarity: 37.6%      Mismatches: 124
Query Match:      33.9%      Indels:      96
DB:              3          Gaps:      11

US-10-626-126-9 (1-391) x US-09-642-852-6 (1-1335)

Qy 18 LeuAlaPheLeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValValIle 37
Db 109 CTGGCCGGCTCATGGCGCTGCTCATGTCGCCACGGTGCTGGGCAAGCGCTGTCATG 168
Qy 38 LeuAlaPheValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeu 57
Db 169 CTCGCCCTTCGTGGCGGACTCGAGCCTCGCACCCAGACAACTTCTTCTGCTCAACCTC 228
Qy 58 AlaIleSerAspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeu 77
Db 229 GCCATCTCCGACTTCTGCTGGCGGCTTCTGCACTCCACCTGTAATGATACCTAGCTGCTG 288
Qy 78 Phe---AsnTrpAsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeu 96
Db 289 ACAGCGCGCTGGACCTTCGGCGCGGCGCTCTGCAAGCTGTGGCTGTGTAGTGACTACTG 348
Qy 97 LeuCysThrAlaSerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerVal 116
Db 349 CTGTGCACCTCTCTGCTGCTCAACATGCTGCTCATAGCTACGACCGCTTCTCTGCTGCTC 408
Qy 117 SerAsnAlaValArgTyrArgAlaGlnHisThrGlyIleLeuIleValAlaGlnMet 136
Db 409 ACCGAGCGGTCTCATACCGGCGCCAGCAGGCTGACACGGCGGCGGAGTGGCGGAAGATG 468
Qy 137 ValAlaValTrpIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSer 156
Db 469 CTGCTGTGTGGTGTCTGCGCTTCTGCTGTACGACCGACGCCATCTCTG-----AGC 519
Qy 157 TrpIys-----AsnSerThrAsnThrGluGluCysGluProGlyPheVal 171
Db 520 TGGGAGTACCTGTCCGGGGGCGAGCTCCATCCCGAGGGCCACTGCTATGCGGAGTTCTTC 579
Qy 172 ThrGluTrpTyrIleLeuAlaIleThrAlaPheLeuGluPheLeuLeuProValSerLeu 191
Db 580 TACAACTGGTACTTCTTCATCAGCGCTTCCACCGCTGGAGTTCTTACGCCCTTCTCTCAGC 639
Qy 192 ValValTyrPheSerValGlnIleTyr----- 200
Db 640 GTACCTTCTTTACCTCAGCACTACTGMAACATCCAGAGGCGCACCGCGCTCGGCTG 699
Qy 200 ----- 200
Db 700 GATGGGGCTCGAGAGGCGCGCGCCCGAGCCCTCCCGAGGGCCAGCCCTCACCACCC 759
Qy 201 -----TrpSerLeuTrpIysArgGlySerLeuSerArgCysProSerHis 215
Db 760 CCACCGCTGCTGCTGGGGTGTGTGGCAGGAAGGGGCACGGGGAGGGCCATGCCGCTGCAC 819
Qy 216 -----AlaGlyPheIleAlaThrSerSer 223
Db 820 AGGTATGGGTGGGTGAGGGCGCGCGTATAGGCGCTGAGGCGCGGGAGGCGACCTCGGGGGT 879

224 ArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeuProGlyLeu 243
Db 880 GCGCGTGGGGCGGCTCC-----GTGGCTTCACCCACCTCCAGCTCCGGC----- 924
Qy 244 LysGluProAlaAsrLeuHisSerGluSerProArgGlyLysSerSerLeuLeuVal 263
Db 925 -----AGCTCTCTGAGGGGCACTGAGAGGGCGCGC----- 954
Qy 264 SerLeuArgThrHisMetSerGlySerIleAlaPheLysValGlySerPheCysArg 283
Db 955 -----TCACTCAAGAGGGGCTCCAAAGCCGCTCG 981
Qy 284 SerGluSerProValLeuHisGlnArg-----GluHis 294
Db 982 GCGTCTGGCGCTCGCTGGAGAGCGCATGAGATGTGTGCCAGAGCTTCACCACCGGC 1041
Qy 295 ValGluLeuLeuArgGlyArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPhe 314
Db 1042 TTTCCGGCTGTCTCGGACAGGAAAGTGCCCAAGTCGCTGGCGCTCATCGTGAGCATCTTT 1101
Qy 315 AlaIleCysTrpAlaProTyrCysLeuPheThrIleValLeuSerThrTyrArgArgGly 334
Db 1102 GGGCTCTGCTGGGCGCCCATACAGCTGCTGATGATCATCCGGCGCGCTGC---CATGGC 1158
Qy 335 GluArgProLysSerIleTrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeu 354
Db 1159 CACTGCGTCCCTGACTACTGCTAGAAACCTCTCTTGGCTCTGTGGCGCACTCGGCT 1218
Qy 355 IleAsnProPheLeuTyrProLeuCysHisArgPheGlnLysAlaPheTrpLysIle 374
Db 1219 GTCAACCTCTCTCTACCTCTGTGCCACACAGCTTCGCGGGGCTTCACCAGCTG 1278
Qy 375 LeuCysValThrIys-----GlnProAlaProSer 384
Db 1279 CTCTGCCCGCAGAAAGCTCAAAATCCAGCCCAACAGCTCC 1317

RESULT 10
US-09-891-053-21
; Sequence 21, Application US/09891053
; Patent No. 6750322
; GENERAL INFORMATION:
; APPLICANT: Itadani, Hiraku
; APPLICANT: Takimura, Tetsuo
; APPLICANT: Nakamura, Takao
; APPLICANT: Kobayashi, Masahiko
; APPLICANT: Tanaka, Ken-ichi
; APPLICANT: Hidaka, Yusuke
; APPLICANT: Ohta, Masataka
; TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)
; TITLE OF INVENTION: BINDING PROTEIN-COUPLED RECEPTOR PROTEINS
; FILE REFERENCE: 06501-083001
; CURRENT APPLICATION NUMBER: US/09/891,053
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: PCT/JP99/07280
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: PCT/JP98/05967
; PRIOR FILING DATE: 1998-12-25
; PRIOR APPLICATION NUMBER: JP 11/145661
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 2050
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (271) ... (1629)
US-09-891-053-21

Alignment Scores:      1.66e-60      Length:      2050
Pred. No.:              693.00      Matches:      163
Score:
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Percent Similarity: 49.2% Conservative: 50
Best Local Similarity: 37.6% Mismatches: 124
Query Match: 33.9% Indels: 96
DB: 3 Gaps: 11

US-10-626-126-9 (1-391) x US-09-891-053-21 (1-2050)

QY 18 LeuAlaPheLeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAenAlaValIle 37
DB CTGGCGGCTCATGGCGTCTCATCGTCCACGCGTGTGGCAACGGCGTGCATG 438
QY 38 LeuAlaPheValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeu 57
DB CTGGCGTCTGTGGCGCACTCGAGCTCCGACCCAGACCAACTTCTTCTGTCTCAACCTC 498
QY 58 AlaIleSerAspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeu 77
DB GCCATCTCCGACTTCTCTGCGGCGCTTCTGCATCCCACTGATGATGATGATGATGATG 558
QY 78 Phe---AsnTrpAsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeu 96
DB ACAGGCGCTGGACCTTCGGCGGGGCTCTGCAAGCTGTGGTGTGGTGTGGTGTGGTGTGG 618
QY 97 LeuCysThrAlaSerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerVal 116
DB CTGTGCACCTCTCTGCTTCAACATCGTCTCATCAGCTACGACCGCTTCTGTGTGGTC 678
QY 117 SerAsnAlaValArgTyrArgAlaGlnHisThrGlyIleLeuIleValAlaGlnMet 136
DB ACCCGAGCGGTCTCATACCGGGGCCAGCAGGGTGACACGCGGGCGGCGGTGCGGAAGATG 738
QY 137 ValAlaValTrpIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSer 156
DB CTGCTGTGTGGTGTGGCTTCTCTGTCTGACGACCAACCCATCTCTG-----AGC 789
QY 157 TrpLys-----AsnSerThrAsnThrGluGluCysGluProGlyPheVal 171
DB TGGAGTACCTGTCCGGGGCGAGCTCCATCCCGAGGGCCACTGCTATGCGCGATCTTCTC 849
QY 172 ThrGluTrpTyrIleLeuAlaIleThrAlaPheLeuGluPheLeuProValSerLeu 191
DB TACAACCTGGTACTTCTCTCATCAGGCTTCCACCTGGAGTTCTTACGGCCCTTCTCTCAGC 909
QY 192 ValValTyrPheSerValGlnIleTyr----- 200
DB GTACCTTCTTTAACCTACGATCTACTGAAATCCAGAGGCGCACCCGCTCCGGCTG 969
QY 200 ----- 200
DB GATGGGCTCGAGAGGCGCGCGCGCGCCCTCCCGAGGCCCGAGCCCTCACCACCC 1029
QY 201 -----TrpSerLeuTyrPheArgGlySerLeuSerArgCysProSerHis 215
DB ----- 1030
DB CCACCGCTGGCTGTGGGCTGTGTGGCAGAGGGCGACGGGAGGCGCATGCGCTGCAC 1089
QY 216 -----AlaGlyPheIleAlaThrSerSer 223
DB AGGTATGGGTGGTGTGGGCGCGGTATGGCGTGTAGGCGCGGGAGGGACCCCTCGGGGT 1149
QY 224 ArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeuProGlyLeu 243
DB GGCGGTGGGGCGGCTCC-----GTGGCTTACCCACCTCCAGCTCCGCGC--- 1194
QY 244 LysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSerLeuVal 263
DB -----AGCTCTCGAGGGGCACTGAGAGGCGCGCGC----- 1224
QY 264 SerLeuArgThrHisMetSerGlySerIleIleAlaPheLysValGlySerPheCysArg 283
DB -----TCACCTCAGAGGGGCTCCAGCCGCTCG 1251
QY 284 SerGluSerProValLeuHisGlnArg-----GluHis 294
DB ----- 1251

1252 GCGTCTCTCGGCTCGCTGGAGAACCCATGAAGATGGTGTCCAGAGCTTACCCAGCGC 1311
295 ValGluLeuLeuArgGlyArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPhe 314
1312 TTTCGGCTGTCTCGGACAGGAAGTGGCAAGTCCGCTGGCCGTCTCATGTGAGCATCTT 1371
315 AlaIleCysTrpAlaProTyrCysLeuPheThrIleValLeuSerThrTyrArgArgGly 334
1372 GGCTCTGTGGGCGCCCATACACGCTGTGATGATCATCCGGCGCGCTGC---CATGGC 1428
335 GluArgProLysSerIleTrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeu 354
1429 CACTGGCTCCCTGACTACTGGTACGAAACCTCTTCTGGCTCTGTGGGCGCAACTGGCT 1488
355 IleAsnProPheLeuTyrProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIle 374
1489 GTCACCCCTGTCTCTACCTCTGTGTCGCCACACAGCTTCCGGCGGGGCTTCCACAGCTG 1548
375 LeuCysValThrLys-----GlnProAlaProSer 384
1549 CTCTGCCCGCAGAAGCTCAAAATCCAGCCCGCACAGCTCC 1587

RESULT 11
US-09-949-016-5059
; Sequence 5059, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 5059
; LENGTH: 2665
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5059

Alignment Scores:
Pred. No.: 2,55e-60 Length: 2665
Score: 693.00 Matches: 163
Percent Similarity: 49.2% Conservative: 50
Best Local Similarity: 37.6% Mismatches: 124
Query Match: 33.9% Indels: 96
DB: 3 Gaps: 11

US-10-626-126-9 (1-391) x US-09-949-016-5059 (1-2665)

QY 18 LeuAlaPheLeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAenAlaValIle 37
DB CTGGCGGCTCATGGCGTCTCATCGTCCACGCGTGTGGCAACGGCGTGCATG 459
QY 38 LeuAlaPheValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeu 57
DB CTGGCGTCTGTGGCGCACTCGAGCTCCGACCCAGACCAACTTCTTCTGTCTCAACCTC 519
QY 58 AlaIleSerAspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeu 77
DB GCCATCTCCGACTTCTCTGCGGCGCTTCTGCATCCCACTGATGATGATGATGATGATG 579
QY 78 Phe---AsnTrpAsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeu 96
DB ACAGGCGCTGGACCTTCGGCGGGGCTCTGCAAGCTGTGGTGTGGTGTGGTGTGGTGTGG 639
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QY 97 LeuCyThrAlaSerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerVal 116
Db 640 CTGTGACCTCTCTGCTGCTCAACATGCTGCTACAGCTACGACCGCTTCTGTGCGTC 699
QY 117 SerAsnAlaValArgTyrArgAlaGlnHisThrGlyIleLeuIleValAlaGlnMet 136
Db 700 ACCGAGCGGTCTCATACCGGGCCACAGCGGTGACACGGCGGCGAGTGGCGAAGATG 759
QY 137 ValAlaValTyrIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSer 156
Db 760 CTGCTGTGTGGGTGCTGCGCTTCTGCTGTACGACCGACCATCTCTG-----AGC 810
QY 157 TrpLys-----AenSerThrAsnThrGluGluCysGluProGlyPheVal 171
Db 811 TGGAGTACCTGTCCGGGGGCGCTCATCCCGAGGGCCACTGCTATGCGGAGTTCTTC 870
QY 172 ThrGluTrpTyrIleLeuAlaIleThrAlaPheLeuGluPheLeuProValSerLeu 191
Db 871 TACAACCTGGTACTTCTCATCAGCGCTTCCACCGCTGGAGTTCTTTACGCGCTTCTCTCAGC 930
QY 192 ValValTyrPheSerValGlnIleTyr----- 200
Db 931 GTCACTTCTTTAACTCAGCATCTACTGAACATCCAGAGGCGCACCCGCTCCGGCTG 990
QY 200 ----- 200
Db 991 GATGGGGCTCAGAGGCGAGCGGGCCCGCGAGCCCTCCCGAGGCCACCGCTCACCACCC 1050
QY 201 -----TtpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHis 215
Db 1051 CCACCGCTGGCTGCTGGGCTGTGTCAGAGGGGCGACGGGAGGCGCATCGCTGCAC 1110
QY 216 -----AlaGlyPheIleAlaThrSerSer 223
Db 1111 AGGTATGGGTGGGTGAGGGCGCGTAGGGCGCTGAGCGCGGGAGGCGACCTCGGGGT 1170
QY 224 ArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeuProGlyLeu 243
Db 1171 GCGGTGGGGGGCGGCTCC-----TGCGCTTCAACCCACCTCCAGCTCCGCGC--- 1215
QY 244 LysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSerLeuVal 263
Db 1216 -----AGTCCTCGAGGGGCACTGAGAGGCGCGC----- 1245
QY 264 SerLeuArgThrHisMetSerGlySerIleAlaPheLysValGlySerPheCysArg 283
Db 1246 -----TCACTCAAGAGGGGCTCAAAGCGCTCG 1272
QY 284 SerGluSerProValLeuHisGlnArg-----GluHis 294
Db 1273 GCGTCTCGGCTCCTCACTGGAGAGCGCATGAAGATGGTGTCCAGAGCTTCAACCCAGCGC 1332
QY 295 ValGluLeuLeuArgGlyArgLysLeuAlaArgSerLeuAlaValLeuSerAlaPhe 314
Db 1333 TTTGCGGTGTCTGGGACAGAAAGTGCCCAAGTGGTGGCTGCGCTCATCGTGAAGATCTTT 1392
QY 315 AlaIleCysTrpAlaProTyrCysLeuPheThrIleValLeuSerThrTyrArgArgGly 334
Db 1393 GGGCTGTGCTGGGCCCCATACACGCTGCTGATCATCATCGGCGCGGCTC---CATGGC 1449
QY 335 GluArgProLysSerIleTrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeu 354
Db 1450 CACTGCGTCCCTGACTACTGTGTACGAAACCTCTCTTCTGGCTCTCTGTGGCGCAACTCGGCT 1509
QY 355 IleAsnProPheLeuTyrProLeuCysHisArgPheGlnLysAlaPheTrpLysIle 374
Db 1510 GTCAACCTGTCTCTACCTCTGTGTCCACACAGCTTCCGCGGGCGCTTCAACAGCTG 1569
QY 375 LeuCysValThrLys-----GlnProAlaProSer 384
Db 1570 CTCTGCCCCAGAGCTCAAAATCCAGCCCCACAGCTCC 1608
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RESULT 12

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US-08-985-090-1
; Sequence 1, Application US/08985090
; Patent No. 5885893
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl
; TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,090
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jean M. Silveri
; REGISTRATION NUMBER: 39,030
; REFERENCE/DOCKET NUMBER: MNI-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2689 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 291..1625
; US-08-985-090-1

Alignment Scores:
Pred. No.: 2,59e-60 Length: 2689
Score: 693.00 Matches: 163
Percent Similarity: 49.2% Conservative: 50
Best Local Similarity: 37.6% Mismatches: 124
Query Match: 33.9% Indels: 96
DB: 2 Gaps: 11

US-10-626-126-9 (1-391) x US-08-985-090-1 (1-2689)
QY 18 LeuAlaPheLeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValIle 37
Db 399 CTGGCGCGCTCATGCGCTGCTCATGCGGCACCGTGTGGCAACGCGCTGTCATG 458
QY 38 LeuAlaPheValAlaAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeu 57
Db 459 CTGCGCTTGTGGCCGACTCGAGCCTCCGACCCAGACCAACTTCTTCTGCTCAACCTC 518
QY 58 AlaIleSerAspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeu 77
Db 519 GCCATCTCCGACTTCTCTGTCGCGCGCTTCTGCATCCCATGTATGTACCTAGTGTCTG 578
QY 78 Phe---AsnTrpAsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeu 96
Db 579 ACAGGCGCTGGACCTTCGGCGCGGCTTCAAGCTGTGGCTGTGGTGTAGTGAGTACCTG 638
QY 97 LeuCyThrAlaSerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerVal 116
Db 639 CTGTGACCTCTCTGCTTCAACATCGTGTCTCATCAGCTACGACCGCTTCTGTGCGTC
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Db 699 ACCGAGCGGTCTATACCGGCGCCAGAGGGTGACAGCGCGGGCGGTGCGGAGATG 758
Qy 137 ValAlaValTrpIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSer 156
Db 759 CTGCTGGTGTGGGTCTGCTGCTGCTAGCAGCAGCAGCATCTG-----AGC 809
Qy 157 TrpLys-----AsnSerThrAsnThrGluGluCysGluProGlyPheVal 171
Db 810 TGGAGTACCTGTCGGGGGCGAGTCCATCCCGAGGGCCACTGATGCGGAGTTCTTC 869
Qy 172 ThrGluTrpTrpIleLeuAlaPheLeuGluPheLeuLeuProValSerLeu 191
Db 870 TACAACTGGTACTCTCATCAGCGCTTCCACCTTGGAGTTCTTACGCCCTTCTCAGC 929
Qy 192 ValValTrpPheSerValGlnIleTyr----- 200
Db 930 GTACCTTCTTTAACTCAGCATCTACCTGAACATCCAGAGCGCACCGCGCTCGGGGTG 989
Qy 200 ----- 200
Db 990 GATGGGCTCGAGAGCGAGCGCGCCCGAGCCCTCCCGAGGCCAGCCCTCACCAACC 1049
Qy 201 -----TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHis 215
Db 1050 CCACCGCTGCTGCTGGGGTCTGTGCAGAGAGGGGACAGGGGAGCGCATGCCCTGCAC 1109
Qy 216 -----AlaGlyPheIleAlaThrSerSer 223
Db 1110 AGGTATGGGTGGGTAGGCGCGGTAGCGCTGAGCGCGGGGAGCGGACCTCGGGGT 1169
Qy 224 ArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeuProGlyLeu 243
Db 1170 GCGGCTGGGGCGGCTCC-----GTGGCTTCAACCCACCTCCAGTCCGGC--- 1214
Qy 244 LysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSerLeuVal 263
Db 1215 -----AGCTCTCGAGGGGCACTGAGAGCGCGC----- 1244
Qy 264 SerLeuArgThrHisMetSerGlySerIleAlaPheLysValGlySerPheCysArg 283
Db 1245 -----TCACCTCAGAGGGGCTCCAGCCGCTG 1271
Qy 284 SerGluSerProValLeuHisGlnArg-----GluHis 294
Db 1272 GCGTCTCGGCTCACTGGAGAGCGCATGAAGATGGTGTCCAGAGCTTCACCCAGCGC 1331
Qy 295 ValGluLeuArgGlyArgGlyLeuAlaArgSerLeuAlaValLeuLeuSerAlaPhe 314
Db 1332 TTTCGGCTGTCTCGGACAGGAAAGTGCCAAAGTGGCTGCGCGCTCATCGTGAATCTTT 1391
Qy 315 AlaIleCysTrpAlaProTyrCysLeuPheThrIleValLeuSerThrTyrArgGly 334
Db 1392 GGGCTGTCTGGGCGCCATACACGCTGCTGATGATCATCGGGCGGCTGC---CATGGC 1448
Qy 335 GluArgProLysSerIleTrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeu 354
Db 1449 CACTGCTCCCTGACTACTGGTACAAACCTCTCTGGCTCTGCTGGCGCAACTCGCT 1508
Qy 355 IleAsnProPheLeuTrpProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIle 374
Db 1509 GTCAACCTGTGCTCTACCTCTGTGTCACACACAGCTTCGCGCGGGCTTCACCAAGCTG 1568
Qy 375 LeuCysValThrLys-----GlnProAlaProSer 384
Db 1569 CTCTGCCCCCAGAGCTCAAAATCCAGCCCCACAGCTCC 1607
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RESULT 14

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US-09-167-354-5
; Sequence 5, Application US/09167354A
; Patent No. 6136559
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
```

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; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; FILE REFERENCE: SUBTYPE
; CURRENT APPLICATION NUMBER: US/09/167,354A
; CURRENT FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 5
; LENGTH: 2699
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDNA
US-09-167-354-5
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Alignment Scores:
Pred. No.: 2,6e-60 Length: 2699
Score: 693.00 Matches: 163
Percent Similarity: 49.2% Conservative: 50
Best Local Similarity: 37.6% Mismatches: 124
Query Match: 33.9% Indels: 96
DB: 3 Gaps: 11

US-10-626-126-9 (1-391) x US-09-167-354-5 (1-2699)
Qy 18 LeuAlaPheLeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValIle 37
Db 407 CTGGCGCGCTCATGGCGCTGCTCATCGTGCCACGGTGTGGGCAACGCGCTGTCATG 466
Qy 38 LeuAlaPheValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeu 57
Db 467 CTGCGCTCTGTGGCGGACTCGAGCTCCGACCCAGAACAACTTCTTCTCTCAACCTC 526
Qy 58 AlaIleSerAspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeu 77
Db 527 GCCATCTCCGACTTCTCGTGGCGCTTCTGCAATCCACTGTATGTACCTACGTGCTG 586
Qy 78 Phe---AsnTrpAsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeu 96
Db 587 ACAGGCGCTGGACCTTCGGCGGGGCTCTGCAAGCTGTGGTGTAGTACGACTACCTG 646
Qy 97 LeuCysThrAlaSerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerVal 116
Db 647 CTGTGCACTCTCTGCTTCAACATCGTCTCATCAGCTACGACCGCTTCTCTCGGTC 706
Qy 117 SerAsnAlaValArgTyrArgAlaGlnHisThrGlyLeuLysIleValAlaGlnMet 136
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Qy 137 ValAlaValTrpIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSer 156
Db 767 CTGCTGTGTGGTGTGGCTTCTCTGCTGTACGACCAAGCATCTCTG-----AGC 817
Qy 157 TrpLys-----AsnSerThrAsnThrGluGluCysGluProGlyPheVal 171
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Qy 172 ThrGluTrpTrpIleLeuAlaIleThrAlaPheLeuGluPheLeuProValSerLeu 191
Db 878 TACAACTGGTACTTCTCTCATCAGCGCTTCCACCTGGAGTTCTTTTACGCCCTTCTCAGC 937
Qy 192 ValValTrpPheSerValGlnIleTyr----- 200
Db 938 GTACCTTCTTTAACTCAGCATCTACCTGAACATCCAGAGGGCGCACCGCGCTCGGGCTG 997
Qy 200 ----- 200
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Qy 201 -----TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHis 215
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Qy 216 -----AlaGlyPheleAlaThrSerSer 223
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Qy 224 ArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeuProGlyLeu 243
Db 1178 GCGGTGGGGGGCGCTCC-----GTGGCTTCACCCACCTCCAGCTCCGGC--- 1222
Qy 244 LysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerLeuLeuVal 263
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Qy 264 SerLeuArgThrHisMetSerGlySerIleAlaPheLysValGlySerPheCysArg 283
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Qy 284 SerGluSerProValLeuHisGlnArg-----GluHis 294
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Qy 315 AlaIleCysTrpAlaProTyrCysLeuPheThrIleValLeuSerThrTyrArgArgGly 334
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Qy 335 GluArgProLysSerIleTrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeu 354
Db 1457 CACTGGCTCCCTGACTACTGGTACGAAACCTCTCTTGGCTCTGTGGCGCAACTGGCT 1516
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Qy 375 LeuCysValThrLys-----GlnProAlaProSer 384
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; Sequence 5, Application US/09642855
; Patent No. 6413743
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; FILE REFERENCE: JMW
; CURRENT APPLICATION NUMBER: US/09/642,855
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: 09/167,354
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 2699
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDNA
US-09-642-855-5
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Pred. No.: 2,6e-60 Length: 2699
Score: 693.00 Matches: 163
Percent Similarity: 49.2% Conservative: 50

Best Local Similarity: 37.6% Mismatches: 124
Query Match: 33.9% Indels: 96
DB: 3 Gaps: 11
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Qy 38 LeuAlaPheValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeu 57
Db 467 CTGGCTCTGGTGGCGGCACTCGAGCTCCGACCCAGACAACTTCTTCTGCTCAACCTC 526
Qy 58 AlaIleSerAsnPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeu 77
Db 527 GCCATCTCGACTTCTCTGTCGGCGCTTCTGTGATCCCACTGATGATGACTACGTGCTG 586
Qy 78 Phe---AsnTrpAsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeu 96
Db 587 ACAGGCGCGCTGGACCTTCGGCGGGGCTCTGCAAGCTGTGGCTGTAGTGAGTACTACCTG 646
Qy 97 LeuCysThrAlaSerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerVal 116
Db 647 CTGTGACCTCTCTGCTTCAACATCGTGTCTCATCAGCTTACGACGCTTCTGTCGGTC 706
Qy 117 SerAsnAlaValArgTyrArgAlaGlnHisThrGlyIleLeuLysIleValAlaGlnMet 136
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Qy 157 TrpLys-----AsnSerThrAsnThrGluGluCysGluProGlyPheVal 171
Db 818 TGGGAGTACCTGTTCGGGGGCGACCTCATCCCGAGGGCCACTGTCTATGCGAGTTCTTC 877
Qy 172 ThrGluTrpTrpIleLeuAlaIleThrAlaPheLeuGluPheLeuProValSerLeu 191
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Db 938 GTACCTCTTTAACTCATGACATCTACTGAAACATCCAGAGGCGCACCCGCTCCGGCTG 997
Qy 200 ----- 200
Db 998 GATGGGCTCGAGAGGCGAGCGCGCCCGAGCCCTCCCGAGGCCACCGCTCACCAACC 1057
Qy 201 -----TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHis 215
Db 1058 CCACCGCTGGTGTGGGGCTCTGCGCAGAGGGGACCGGGAGGCGCATGCGCTGCAC 1117
Qy 216 -----AlaGlyPheIleAlaThrSerSer 223
Db 1118 AGGTATGGGTGGGTGAGCGCGCTAGGCGCTGAGCGGGGAGGCGACCTCGGGGT 1177
Qy 224 ArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeuProGlyLeu 243
Db 1178 GCGGTGGGGGGCGCTCC-----GTGGCTTCACCCACCTCCAGCTCCGGC--- 1222
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Qy 264 SerLeuArgThrHisMetSerGlySerIleIleAlaPheLysValGlySerPheCysArg 283
Db 1253 -----TCACTCAAGAGGGGCTCCAAAGCCGTGC 1279
Qy 284 SerGluSerProValLeuHisGlnArg-----GluHis 294
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Qy 315 AlaIleCysTrpAlaProTyrCysLeuPheThrIleValLeuSerThrTyrArgArgGly 334
Db 1400 GGGCTCTGCTGGGCCCCATACACGCTGCTGATGATCATCCGGCGCGCTGC---CATGGC 1456
Qy 335 GluArgProLysSerIleTyrTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeu 354
Db 1457 CACTGCGTCCCTGACTACTGTGTACGAAACCTCTCTGGCTCTCTGGGCCCACTCGGCT 1516
Qy 355 IleAsnProPheLeuTyrProLeuCysHisArgArgPheGlnLysAlaPheTrpIle 374
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Qy 375 LeuCysValThrLys-----GlnProAlaProSer 384
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Job time : 262 secs

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GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 29, 2006, 01:58:11 ; Search time 861 Seconds
(without alignments)
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Perfect score: 2045
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
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Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=Published Applications NA.Main -OPMT=fastap -SUFFIX=p2n.rnpbm
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Database : Published Applications NA.Main:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2034	99.5	1176	9	US-10-626-126-6 Sequence 6, Appli
3	2034	99.5	1176	9	US-10-626-398-6 Sequence 6, Appli
4	1742	85.2	1176	8	US-10-626-445-5 Sequence 5, Appli
5	1742	85.2	1176	9	US-10-626-126-5 Sequence 5, Appli
6	1742	85.2	1176	9	US-10-626-398-5 Sequence 5, Appli
7	1403.5	68.6	1170	9	US-10-488-421-7 Sequence 7, Appli

8	1403.5	68.6	1173	3	US-09-812-216-1	Sequence 1, Appli
9	1403.5	68.6	1173	3	US-09-910-411-1	Sequence 1, Appli
10	1403.5	68.6	1173	3	US-09-875-076-13	Sequence 13, Appli
11	1403.5	68.6	1173	3	US-09-876-252-13	Sequence 13, Appli
12	1403.5	68.6	1173	5	US-10-052-193-1	Sequence 1, Appli
13	1403.5	68.6	1173	6	US-10-272-983-13	Sequence 13, Appli
14	1403.5	68.6	1173	6	US-10-354-769-1	Sequence 1, Appli
15	1403.5	68.6	1173	6	US-10-393-807-13	Sequence 13, Appli
16	1403.5	68.6	1173	6	US-10-417-820A-13	Sequence 13, Appli
17	1403.5	68.6	1173	7	US-10-349-253A-1	Sequence 1, Appli
18	1403.5	68.6	1173	7	US-10-723-955-13	Sequence 13, Appli
19	1403.5	68.6	1173	7	US-10-782-596-13	Sequence 13, Appli
20	1403.5	68.6	1173	7	US-10-737-619-1	Sequence 1, Appli
21	1403.5	68.6	1173	8	US-10-626-445-1	Sequence 1, Appli
22	1403.5	68.6	1173	8	US-10-616-088-1	Sequence 1, Appli
23	1403.5	68.6	1173	9	US-10-626-126-1	Sequence 1, Appli
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26	1403.5	68.6	1266	3	US-09-891-138A-5	Sequence 5, Appli
27	1403.5	68.6	1300	3	US-09-852-165-1	Sequence 1, Appli
28	1403.5	68.6	1300	7	US-10-696-673-1	Sequence 1, Appli
29	1403.5	68.6	3689	5	US-10-225-567A-628	Sequence 628, App
30	1403.5	68.6	3689	8	US-10-684-206-19	Sequence 19, Appli
31	1403.5	68.6	3689	9	US-10-756-149-32	Sequence 32, Appli
32	1398.5	68.4	1173	6	US-10-230-078-26	Sequence 26, Appli
33	1398.5	68.4	1265	9	US-10-488-421-5	Sequence 25, Appli
34	1398.5	68.4	1265	9	US-10-626-445-7	Sequence 7, Appli
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36	1237.5	60.5	1170	9	US-10-626-398-7	Sequence 7, Appli
37	1237.5	60.5	1170	9	US-10-488-421-3	Sequence 3, Appli
38	1233	60.3	1166	9	US-10-488-421-1	Sequence 1, Appli
39	1117.5	54.6	1103	9	US-09-350-206-3	Sequence 3, Appli
40	693	33.9	1335	3	US-09-349-755-3	Sequence 3, Appli
41	693	33.9	1335	3	US-09-166-334-3	Sequence 3, Appli
42	693	33.9	1335	5	US-10-282-958-3	Sequence 3, Appli
43	693	33.9	1335	7	US-10-727-021-6	Sequence 6, Appli
44	693	33.9	1335	10	US-11-059-105-3	Sequence 3, Appli
45	693	33.9	1335	10	US-11-059-105-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1

US-10-626-445-6
; Sequence 6, Application US/10626445
; Publication No. US20040248252A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0032
; CURRENT APPLICATION NUMBER: US/10/626, 445
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 6
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Rattus rattus
US-10-626-445-6

Alignment Scores:
Pred. No.: 5.75e-215 Length: 1176
Score: 2034.00 Matches: 390
Percent Similarity: 99.7% Conservatives: 0
Best Local Similarity: 99.7% Mismatches: 1
Query Match: 99.5% Indels: 0
DB: 8 Gaps: 0

US-10-626-126-9 (1-391) x US-10-626-445-6 (1-1176)

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QY 21 LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValValIleLeuAlaPhe 40
DB 61 TTAATGTCCTGCTTGCTTTGCTATACGATAGGCATGCTGTGGTCATTTTAGCCTT 120
QY 41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
DB 121 GTAGCAGACAGAAACCTTACACATCGAAGTAATATATTTTCTTAATTTGGCTATTCT 180
QY 61 AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTrp 80
DB 181 GACTTCTTCGTGGGTGTCATCTCCATTCCTCTGTACATCCTCACACGCTGTTAACTGG 240
QY 81 AsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100
DB 241 AATTTTGGAAAGTGAATCTGCATGTTTGGCTCATTTACTGACTATCTTTTGTGCACAGCA 300
QY 101 SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
DB 301 TCCGTCTACAGTATTGCTCCTCATTAGCTACGATACGATACAGTCAGTTTCAAACGCTGTG 360
QY 121 ArgTyrArgAlaGlnHisThrGlyIleLeuIleValAlaGlnMetValAlaValTrp 140
DB 361 CGTTATAGACACAGCACACTGGCATCTCGAATAATTTGCTCAAAATGGTGGTGTGG 420
QY 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160
DB 421 ATACTGGCTTTCTTGGTCAATGGCCCAATGATTCTGGCTTCGGATTCTTGGAGAACAGC 480
QY 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTrpTyrIleLeuAlaIleThr 180
DB 481 ACCACACACAGGAGTGGAGCCTGGCTTGTGTACTGAGTGGTACATCCTCGCCATTACA 540
QY 181 AlaPheLeuGluPheLeuLeuProValSerLeuValValTyrPheSerValGlnIleTyr 200
DB 541 GCATTCTTGGAAATTCCTGCTCCCTGCTCCTTGGTGTCTATTTCAGTGTACAGATTAC 600
QY 201 TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220
DB 601 TGGAGCCTGTGGAAAGCTGGAGTCTCAGTAGGTGCCCTAGCCACCGCTGGATTATCGCT 660
QY 221 ThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu 240
DB 661 ACCTCTTCCAGGGGCACCTGGACACTCACGCAGAACTGGGTGGCTTTAGACACAAGTCTT 720
QY 241 ProGlyLeuLysGluProAlaIleSerLeuHisSerGluSerProArgGlyLysSerSer 260
DB 721 CCTGGATTAAAGGAACAGCGCATCCTCTTCATTCAGAAAGTCCACGAGGAAAGAGCAGT 780
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DB 841 TTCTGCCGATCAGAAAGCCAGTCGCTTCCACGAGAGAGCAGCTGGAGCTTCTCAGAGGC 900
QY 301 ArgLysLeuAlaArgSerLeuAlaValLeuSerAlaPheAlaIleCysTrpAlaPro 320
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QY 381 ProAlaProSerGlnThrGlnSerValSerSer 391
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RESULT 2

US-10-626-126-6
; Sequence 6, Application US/10626126
; Publication No. US20050074770A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0033
; CURRENT APPLICATION NUMBER: US/10/626,126
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Rattus rattus
US-10-626-126-6

Alignment Scores:
Pred. No.: 5,75e-215 Length: 1176
Score: 2034.00 Matches: 390
Percent Similarity: 99.7% Conservative: 0
Best Local Similarity: 99.7% Mismatches: 1
Query Match: 99.5% Indels: 0
DB: 9 Gaps: 0

US-10-626-126-9 (1-391) x US-10-626-126-6 (1-1176)

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DB 1 ATGTCGGAGTCTAAACGGCAGCTGCTGCCACGTGCTCAAGTCCCTTTGGCATT 60
QY 21 LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValValIleLeuAlaPhe 40
DB 61 TTAATGTCCTGCTTGCTTTGCTATAACGATAGGCATGCTGTGGTCATTTTAGCCTTT 120
QY 41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
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QY 61 AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTrp 80
DB 181 GACTTCTTCGTGGGTGTCATCTCCATTCCTCTGTACATCCTCACACGCTGTTAACTGG 240
QY 81 AsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100
DB 241 AATTTTGGAAAGTGAATCTGCATGTTTGGCTCATTTACTGACTATCTTTTGTGCACAGCA 300
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DB 301 TCCGTCTACAGTATTGCTCCTCATTAGCTACGATACGATACAGTCAGTTTCAAACGCTGTG 360
QY 121 ArgTyrArgAlaGlnHisThrGlyIleLeuLysIleValAlaGlnMetValAlaValTrp 140
DB 361 CGTTATAGACACAGCACACTGGCATCTCGAATAATTTGCTCAAAATGGTGGTGTGG 420
QY 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160
DB 421 ATACTGGCTTTCTTGGTCAATGGCCCAATGATTCTGGCTTCGGATTCTTGGAGAACAGC 480
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Qy 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTrpTyrIleLeuAlaIleThr 180
Db 481 ACCAACACAGAGGAGTGGAGCCCTGGCTTTGTACTAGTGGTACATCCCTCGCCATTACA 540
Qy 181 AlaPheLeuGluPheLeuLeuProValSerLeuValValTyrPheSerValGlnIleTyr 200
Db 541 GCATTCCTGGGATTCCTGCTCCCTGTCTCTTGGTGGTCTATTATTCAGTGATACAGATTAC 600
Qy 201 TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220
Db 601 TGGAGCCCTGTGGAAGCGTGGAGTCTCAGTAGGTGCTCAGAGTGGCTTAGCCACCGCTCATCGCT 660
Qy 221 ThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu 240
Db 661 ACCTCTTCCAGGGGCATGGACATCCACGCAGAACTGGGTGGCTTGTAGGACAAAGTCTT 720
Qy 241 ProGlyLeuLysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSer 260
Db 721 CCTGGATTAAAGGAACCCAGCGCATCCCTTCATTAGAAAGTCCACGAGGAAAGAGCAGT 780
Qy 261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleIleAlaPheLysValGlySer 280
Db 781 CTCCTGGTGTCTTAAGGACTCACATGAGCGGTAGTATCATCGGCTTCAAAGTGGGTTC 840
Qy 281 PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300
Db 841 TTCTGCGCATCAGAAAGCCAGTGTCTTCCAGAGAGAGCAGCGTGGAGCTTCTCAGAGGC 900
Qy 301 ArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
Db 901 AGGAAGCTAGCCAGTCCGTAGCTGTCTCTCTAGTGTCTTTTGGCAATTCCTGGGTCCG 960
Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle 340
Db 961 TATTGCTGTTCACAAATTGCTTTTCACTTATCGAGAGGGAGCGCCCAATCGATT 1020
Qy 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnProPheLeuTyr 360
Db 1021 TGGTACAGCATAGCCTTTTGGCTACAGTGGTTCAAATTCACCTATTAAATCCCTTCTATAC 1080
Qy 361 ProLeuCysHisArgGlyPheGlnLysAlaPheTrpLysIleLeuCysValThrLysGln 380
Db 1081 CCTTTGGCCACAGACGTTTCCAGAAAGCTTTCTGGAAAGATACTCTGTGTGACAAAGCAA 1140
Qy 381 ProAlaProSerGlnThrGlnSerValSerSer 391
Db 1141 CCAGCACCTTCACAGACCCAGTCAAGTATCTTCT 1173
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RESULT 3

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US-10-626-398-6
; Sequence 6, Application US/10626398
; Publication No. US20050074841A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE OF INVENTION: PRD-0034
; CURRENT APPLICATION NUMBER: US/10/626,398
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Rattus rattus
US-10-626-398-6
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Alignment Scores:

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Pred. No.: 5,75e-215 Length: 1176
Score: 2034.00 Matches: 390
Percent Similarity: 99.7% Conservative: 0
Best Local Similarity: 99.7% Mismatches: 1
Query Match: 99.5% Indels: 0
DB: 9 Gaps: 0

US-10-626-126-9 (1-391) x US-10-626-398-6 (1-1176)

Qy 1 MetSerGluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe 20
Db 1 ATGTGGAGTCTAAACGCACTGACGCTTGGCCACTGACTGCTCAAGTCCCTTGGCAATT 60
Qy 21 LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValValIleLeuAlaPhe 40
Db 61 TTAATGTCCTGCTTGTCTTTTGTCTATAACGATAGGCAATGCTGGGTCATTTTAGCCCTT 120
Qy 41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
Db 121 GTAGCAGACAGAAACCTTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTCT 180
Qy 61 AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTrp 80
Db 181 GACTTCTTCGTGGTGTCACTCCATTCCTCTGTACATCCCTCACACGCTGTTTAACTGG 240
Qy 81 AsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100
Db 241 AATTTTGGAAAGTGGAACTCTGCATGTTTGGCTCATTACTGACTATCTTTTGTGCACAGCA 300
Qy 101 SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
Db 301 TCCGTCTACAGTATTGTCTCATATTAGCTACGATCGATACAGTCAGTTCCTCAAGCTGTG 360
Qy 121 ArgTyrArgAlaGlnHisThrGlyIleLeuLysIleValAlaGlnMetValAlaValTrp 140
Db 361 CGTTATAGACACACAGCACACTGGCATCTCGAAATTTGCTCAAAATGGTGGCTGTTGG 420
Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160
Db 421 ATACTGGCTTTCTTGGTCAATGGCCCAATGATTCGGCTTCGGATTCCTGGAAAGACAGC 480
Qy 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTrpTyrIleLeuAlaIleThr 180
Db 481 ACCAACACAGAGGAGTGGAGCCCTGGCTTTGTACTAGTGGTACATCTCCGCCATTACA 540
Qy 181 AlaPheLeuGluPheLeuLeuProValSerLeuValValTyrPheSerValGlnIleTyr 200
Db 541 GCATTCCTGGAAATTCCTGCTCCCTGCTCTCTTGGTGTCTATTATTCAGTGATACAGATTAC 600
Qy 201 TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220
Db 601 TGGAGCCCTGTGGAAGCGTGGAGTCTCAGTAGGTGCTTACGAGCAGCGCTGGATTCATCGCT 660
Qy 221 ThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu 240
Db 661 ACCTCTTCCAGGGGCATGGACACTCACGCAAGCTGGGTGGCTTGTAGGACAAAGTCTT 720
Qy 241 ProGlyLeuLysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSer 260
Db 721 CCTGGATTAAAGGAACCCAGCGCATCCCTTCATTAGAAAGTCCACGAGGAAAGAGCAGT 780
Qy 261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleIleAlaPheLysValGlySer 280
Db 781 CTCCTGGTGTCTTAAGGACTCACATGAGCGGTAGTATCATCGCTTCAAAGTGGGTTC 840
Qy 281 PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300
Db 841 TTCTGCGCATCAGAAAGCCAGTGTCTTCCAGAGAGAGCAGCGTGGAGCTTCTCAGAGGC 900
Qy 301 ArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
Db 901 AGGAAGCTAGCCAGTCCGTAGCTGTCTCTGAGTGTCTTTTGGCAATTCCTGGGTCCG 960
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Qy 321 TycCysLeuPheThrIleValLeuSerThrTyArgArgGlyGluArgProLysSerIle 340
Db 961 TAITGCCTGTTCAAAATGTTCTTCACTATCGCAGAGGGAGCGCCCAAAATCGAAT 1020
Qy 341 TTPTySerIleAlaPheTTPLeuGlnTTPPheAsnSerLeuIleAsnProPheLeuTyr 360
Db 1021 TGGTACAGCATAGCCTTTTGGCTACAGTGGTTCATTTCACTTATTAATCCCTTTCTATAC 1080
Qy 361 ProLeuCysHisArgArgPheGlnLysAlaPheTTPlysIleLeuCysValThrLysGln 380
Db 1081 CCTTTGGCCACAGACGTTTCCAGAGGCTTTCTGGAGAGATACCTCTGTGTGACAAAGCAA 1140
Qy 381 ProAlaProSerGlnThrGlnSerValSerSer 391
Db 1141 CCAGACCTTTCACAGACCCAGTCAGTATCTTCT 1173

RESULT 4
US-10-626-445-5
; Sequence 5, Application US/10626445
; Publication No. US20040248252A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0032
; CURRENT APPLICATION NUMBER: US/10/626,445
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-626-445-5

Alignment Scores:
Pred. No.: 1,5e-182 Length: 1176
Score: 1742.00 Matches: 332
Percent Similarity: 89.3% Conservative: 17
Best Local Similarity: 84.9% Mismatches: 42
Query Match: 85.2% Indels: 0
DB: 8 Gaps: 0

US-10-626-126-9 (1-391) x US-10-626-445-5 (1-1176)
Qy 1 MetSerGluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe 20
Db 1 ATGTCGGAGTCTAACAGTACTGGCATCTGCCACAGCTGCTCAGGTCCTCCCTGGCATTT 60
Qy 21 LeuMetSerLeuAlaPheAlaIleThrIleGlyAsnAlaValValIleLeuAlaPhe 40
Db 61 TTAATGCTTCAATTCGCTTTGCTAATAATGCTAGGCAATGCTGTGTCATCTTAGCCTTT 120
Qy 41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
Db 121 GTGGTGACAGAAACCTTAGACATCGAAGTAATATTTTCTTAAATTTGGCTATTTCT 180
Qy 61 AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrIleLeuPheAsnTyr 80
Db 181 GACTTCTCGTGGTGTGATTTCAATTCCTCTGTGTACATCCCTCAGCTGTGTTTAACTGG 240
Qy 81 AsnProGlySerGlyIleCysMetPheTTPLeuIleThrAspTyrLeuLeuCysThrAla 100
Db 241 AATTTGGAAGTGAATCTGATGTTTGGCTCATTACTGACTATCTTTTGTGTCACGGCA 300
Qy 101 SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
Db 301 TCTGTCTACAATAATTTGCTCTCATAGTACGATCGATACAGTCAGTTTCAAAATGCTGTG 360
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Qy 121 ArgTyArgAlaGlnHisThrGlyIleLeuLysIleValAlaGlnMetValAlaValTTP 140
Db 361 TCTTAGGGCTCAACACACATCGCATCATCAAGATTGTTGCTCAAAATGGTGTGTTGG 420
Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTTPlysAsnSer 160
Db 421 ATACTGGCTTTCTTGTGTAATGGCCGATGATTTCTGGCTTCAGATTCTTTGAAGAACAGC 480
Qy 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTTPTyIleLeuAlaIleThr 180
Db 481 ACGAACACAAAGGACTGTGAGCTGGCTTTGTTGACAGTGGTACATCTCCACATTACA 540
Qy 181 AlaPheLeuGluPheLeuLeuProValSerLeuValValTyrPheSerValGlnIleTyr 200
Db 541 ATGCTCTTGGAAATTCCTGCTTCCTGTCATCTCTGTGGCTTATTTCAATGTACAGATTAC 600
Qy 201 TTPSerLeuTTPlysArgGlySerLeuSerArgCysProSerHisIleAlaGlyPheIleAla 220
Db 601 TGGAGCCTCTGGAAGCGTAGGGCTCTCAGTAGGTGCCCTAGCCATGCTGGATTCTCCACT 660
Qy 221 ThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu 240
Db 661 ACCTCTTCAGTGTCTTACAGACACTTACACAGAGCTGGGTGGCTTGCAGGACAAATAAT 720
Qy 241 ProGlyLeuLysGluProAlaSerLeuHisSerGluSerProArgGlyLysSerSer 260
Db 721 CCTGGATTGAAGGAATCAGCTGTCATCTGCTCACTCAGAAAGTCTCGAAGAAAGACAGC 780
Qy 261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleIleAlaPheLysValGlySer 280
Db 781 ATCTGTGTCCTTAAAGGACTCACAACAGCAGTATCCTGCTTCAAAAGTGGGTTC 840
Qy 281 PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300
Db 841 TTCGCGCATCGAAAGTGCAGCGCTTCGCCAAAGGAGTACGCCAGAGTCTTCAGAGGC 900
Qy 301 ArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTTPAlaPro 320
Db 901 AGGAAGCTAGCCAGGTCACCTGGCCATCTTCTGAGCGCTTTTGCCATTTGCTGGGTCCA 960
Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle 340
Db 961 TACTGTCTGTTCACAATTTGCTCTTCACTTACCCAGAACCGAACGCCCAAAATCGGTG 1020
Qy 341 TTPTySerIleAlaPheTTPLeuGlnTTPPheAsnSerLeuIleAsnProPheLeuTyr 360
Db 1021 TGTACAGCATTTGCTTCTGGCTGCANUGTTCAATTCCTTTGTTAAUCCCTTCTGTAC 1080
Qy 361 ProLeuCysHisArgArgPheGlnLysAlaPheTTPlysIleLeuCysValThrLysGln 380
Db 1081 CCTTTGTGTACAGCGCTTTCAGAGGCTTTCTGGAAGATACTTTGTGTGACAAAGCAA 1140
Qy 381 ProAlaProSerGlnThrGlnSerValSerSer 391
Db 1141 CCAGCGCTGTCAAGAACCCAGTCAGTATCTTCT 1173

RESULT 5
US-10-626-126-5
; Sequence 5, Application US/10626126
; Publication No. US20050074770A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0033
; CURRENT APPLICATION NUMBER: US/10/626,126
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
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; SEQ ID NO 5
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-626-126-5

Alignment Scores:
Pred. No.: 158-182 Length: 1176
Score: 1742.00 Matches: 332
Percent Similarity: 89.3% Conservatives: 17
Best Local Similarity: 84.9% Mismatches: 42
Query Match: 85.2% Indels: 0
DB: 9 Gaps: 0

US-10-626-126-9 (1-391) x US-10-626-126-5 (1-1176)
Qy 1 MetSerGluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe 20
Db 1 ATGTGGAGTCTAACAGTACTGGCATCTTGCCACCAGCTGCTCAGGTCCCTTGGCATTT 60
Qy 21 LeuMetSerLeuAlaPheAlaIleThrIleGlyAsnAlaValValLeuAlaPhe 40
Db 61 TTAATGTCCTTCAATTTGGCTTATATAGTGGCAATGCTGTGTCATCTTAGCCCTT 120
Qy 41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
Db 121 GTGTGGACAGAAACCTTAGACATCGNAGTAATATATTTTCTTAATTTGGCTATTCT 180
Qy 61 AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTyr 80
Db 181 ATCTGGTGCTCTTAAGGACTCACATGACAGCAGTATCAGTGCCTTCAAAGTGGTCC 840
Qy 281 PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300

; SEQ ID NO 5
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-626-126-9

Alignment Scores:
Pred. No.: 158-182 Length: 1176
Score: 1742.00 Matches: 332
Percent Similarity: 89.3% Conservatives: 17
Best Local Similarity: 84.9% Mismatches: 42
Query Match: 85.2% Indels: 0
DB: 9 Gaps: 0

US-10-626-398-5
; Sequence 5, Application US/10626398
; Publication No. US20050074841A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0034
; CURRENT APPLICATION NUMBER: US/10/626,398
; PRIOR FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-626-398-5

Alignment Scores:
Pred. No.: 158-182 Length: 1176
Score: 1742.00 Matches: 332
Percent Similarity: 89.3% Conservatives: 17
Best Local Similarity: 84.9% Mismatches: 42
Query Match: 85.2% Indels: 0
DB: 9 Gaps: 0

US-10-626-126-9 (1-391) x US-10-626-398-5 (1-1176)
Qy 1 MetSerGluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe 20
Db 1 ATGTGGAGTCTAACAGTACTGGCATCTTGCCACCAGCTGCTCAGGTCCCTTGGCATTT 60
Qy 21 LeuMetSerLeuAlaPheAlaIleThrIleGlyAsnAlaValValLeuAlaPhe 40
Db 61 TTAATGTCCTTCAATTTGGCTTATATAGTGGCAATGCTGTGTCATCTTAGCCCTT 120
Qy 41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
Db 121 GTGTGGACAGAAACCTTAGACATCGNAGTAATATATTTTCTTAATTTGGCTATTCT 180
Qy 61 AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTyr 80
Db 181 GACTTCCTCGTGGGTGATTTCCATTCCTCTGTACATCCCTCAGGTGTTGTTAACTGG 240
Qy 81 AsnProGlySerGlyLeuValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTyr 100
Db 241 AATTTTGGAGTGAATCTGCATGCTTTGGCTCATTACTGACTACTCTTTTGTGACCGCA 300
Qy 101 SerValTyrSerIleValLeuSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
Db 301 TCTGTCTACATAATTTGCTCTATTAGTACCATCGATCCAGTTCAGTTCAAATGCTGTG 360
Qy 121 ArgTyrArgAlaGlnHisThrGlyLeuLysIleValAlaGlnMetValAlaValTyr 140
Db 361 TCTTATAGGCTCAACACACTGGCATCATGAGATTGTTGCTCAATGGTGGCTTTGGT 420
Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTyrLysAsnSer 160
Db 421 ATACTGGCTTTCTGGTAAATGGCCCGCATGATCTGCTTCAGATTCTTGAAGAACAGC 480
Qy 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTyrIleLeuAlaIleThr 180
Db 481 ACGAACACAAAGGACTGTGAGCCCTGGCTTTGTTACAGAGTGTATCATCCTCACCATTTACA 540
Qy 181 AlaPheLeuGluPheLeuLeuProValSerLeuValValTyrPheSerValGlnIleTyr 200
Db 541 ATGCTCTTGGAAATTCCTGCTTCCTGTCATCTCTGGGCTTATTTCAATGTACAGATTAC 600
Qy 201 TrpSerLeuTyrLysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220
Db 601 TGGAGCTGTGGAGCGTAGGGCTCTCAGTAGGTGGCCCTAGCCATGCTGGATTCTCCACT 660
Qy 221 ThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu 240
Db 661 ACCTCTTCCAGTGTCTTCCAGGACACTTACACAGAGCTGGGGTGGCTTCGAGGACAGTAAT 720
Qy 241 ProGlyLeuLysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSer 260
Db 721 CCTGGATTGAAGGAATCAGCTGTCATCTCGTCATCTCAGAAAGTCTCTCGAGGACAGGAGC 780
Qy 261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleIleAlaPheLysValGlySer 280
Db 781 ATCTGGTGCTCTTAAGGACTCACATGACAGCAGTATCAGTGCCTTCAAAGTGGTTC 840
Qy 281 PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300
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Db 241 AATTTTGGAAAGTGAATCTGCATGTTTGGCTCATTACTGACTATCTTTGTGCACGCA 300
Qy 101 SerValTyrSerIleValLeuIleSerTyrAspArgTyrClnSerValSerAsnAlaVal 120
Db 301 TCTGTCTACAAATATGTCCTCATTAGCTAGCATCGATACCAGTCAGTTTCAAAATGCTGTG 360
Qy 121 ArgTyrArgAlaGlnHisThrGlyIleLeuLysIleValAlaGlnMetValAlaValTyr 140
Db 361 TCTTATAGGCTCAACACATCGCATCATGAGATTGTTGCTCAATGGTGGCTGTTGG 420
Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160
Db 421 ATACTGGCTTCTTGGTAATGCCCGCATGATCTCTGGCTTACAGTTCAGATCTTGGAAAGACAGC 480
Qy 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTrpTyrIleLeuAlaIleThr 180
Db 481 ACGAACAACAAAGACTGTGAGCTGGCTTTGTACAGAGTGGTACATCCTCACCATTTACA 540
Qy 181 AlaPheLeuGluPheLeuLeuProValSerLeuValTyrPheSerValGlnIleTyr 200
Db 541 ATGCTCTTGGAAATCTCTGCTTCTGTGCTTATTTCAATGTACAGATTAC 600
Qy 201 TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220
Db 601 TCGAGCCTGTGGAAGCGTAGGCTCTCAGTAGGTGCCCTAGCCATGCTGGATTCTCCACT 660
Qy 221 ThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu 240
Db 661 ACCTCTTCCAGTGCTTACAGACACTTACACAGAGCTGGGTGGCTTGCAGGACAGTAAT 720
Qy 241 ProGlyLeuLysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSer 260
Db 721 CTTGGATTGAGGATCAGCTGATCTCTGTCATCTCAGAAAGTCTCTGAAGAAAGAGCAGC 780
Qy 261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleIleAlaPheLysValGlySer 280
Db 781 ATCTCTGGTGCTTAAGGACTCACATGAACAGCAGTATCACTGCCTTCAAAAGTGGGTTC 840
Qy 281 PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300
Db 841 TTTCTGGCGATCGGAAAGTGCGAGCGCTTCGCCAAAGGGAGTACGACGAGCTTCTCAGAGGC 900
Qy 301 ArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
Db 901 AGAAGCTACCGAGTCACTGGCCATCCTTCTGAGCGCTTTTGCCATTCTGCTGGCTCCA 960
Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle 340
Db 961 TACTGTCTGTTCAATTTGCTTTCACTTACCCAGAACGGAAAGCCCAAAATCGGTG 1020
Qy 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnProPheLeuTyr 360
Db 1021 TGGTACAGCATGCTCTTCTGGCTGCAATGGTTCAATTCGTTGTTATCCCTTTCTGTAC 1080
Qy 361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysGln 380
Db 1081 CCTTTGTGTACAGGCGCTTTCAGAGGCGCTTCTGGAGAGTACTTGTGTGACAAAGCAA 1140
Qy 381 ProAlaProSerGlnThrGlnSerValSerSer 391
Db 1141 CCAGCGCTGTACAGAACCAAGTACGTATCTTCT 1173
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RESULT 7

US-10-488-421-7

; Sequence 7, Application US/10488421

; Publication No. US20050239065A1

; GENERAL INFORMATION:

; APPLICANT: Merck & Co., Inc. [US/US]

; APPLICANT: Gallagher, Michael J.

; APPLICANT: Yates, Stephen L.

; TITLE OF INVENTION: HISTAMINE RECEPTOR H4 POLYNUCLEOTIDES

; FILE REFERENCE: 1367-13335W001

; CURRENT APPLICATION NUMBER: US/10/488,421

; CURRENT FILING DATE: 2004-03-01

; PRIOR APPLICATION NUMBER: US 60/316,762

; PRIOR FILING DATE: 2001-08-31

; PRIOR APPLICATION NUMBER: US 60/332,697

; PRIOR FILING DATE: 2001-11-13

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 7

; LENGTH: 1170

; TYPE: DNA

; ORGANISM: Homo Sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(1170)

; OTHER INFORMATION:

; FEATURE:

; NAME/KEY: misc feature

; OTHER INFORMATION: H4SEQMORSE - Genbank Accession No. AF329449

; FEATURE:

; NAME/KEY: misc feature

; OTHER INFORMATION: Morse, et al., JPET 296(3):1058-1066 (2001); U.S. Patent

; OTHER INFORMATION: No. 6,204,017; WO 01/25432 A2

; FEATURE:

; NAME/KEY: misc feature

; OTHER INFORMATION: Liu - Genbank Accession No. AF312230 - Liu et al., Mol.

; OTHER INFORMATION: Pharmacol 59(3):420-426 (2001)

; FEATURE:

; NAME/KEY: misc feature

; OTHER INFORMATION: Banyu - Genbank Accession No.: AB045370; WO 01/46414 A1

; FEATURE:

; NAME/KEY: misc feature

; OTHER INFORMATION: Nguyen, et al., Mol. Pharmacol 59(3):427-433 (2001) a.a. sequence

; OTHER INFORMATION: only

; FEATURE:

; NAME/KEY: misc feature

; OTHER INFORMATION: Jones - Genbank Accession No.: AF307973; Nucleotides 460-462

; OTHER INFORMATION: are AAG and 988 is C

US-10-488-421-7

Alignment Scores:

Pred. No.: 5,68e-145 Length: 1170

Score: 1403.50 Matches: 271

Percent Similarity: 79.3% Conservative: 40

Best Local Similarity: 69.1% Mismatches: 78

Query Match: 68.6% Indels: 3

DB: 9 Gaps: 2

US-10-626-126-9 (1-391) x US-10-488-421-7 (1-1170)

Qy 1 MetSerGluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe 20

Db 1 ATCCAGATACATAAGCAATCAATTTATCACTAAGCACTCGTTACTTTAGCATTT 60

Qy 21 LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValValIleLeuAlaPhe 40

Db 61 TTTATGTCCTTAGCTAGCTTTTCTATAATGCTAGGAAATGCTTGGTCATTTTAGCTTTT 120

Qy 41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60

Db 121 GTGGTGACAAAAACCTTAGACATCGAAGTAGTTATTTTCTTAACTTGGCCATCTCT 180

Qy 61 AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTrp 80

Db 181 GACTTCTTGTGGGTGGATCTCCATTCCTTTGTACATCCCTCACAGCTGTCGATGG 240

Qy 81 AsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100

Db 241 GATTTTGGAAAGGAATCTGTGATTTTGGCTCACTACTGACTATCTGTATGTACAGCA 300

Qy 101 SerValTyrSerIleValLeuIleSerTyrAspArgTyrClnSerValSerAsnAlaVal 120

Db 301 TCTGTATATAACATTGCTCATCATGATCGATACCTGTCAAGTCTCAAAATGCTGTG 360

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Qy 121 ArgTyrArgAlaGlnHisThrGlyIleLeuLysValAlaGlnMetValAlaValTTP 140
Db 361 TCTTATAGAACTCAACATCTGGGCTCTGAAGATTCTTACTCTGATGGTGGCGTTGG 420
Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAepSerTrpLysAenSer 160
Db 421 GTGCTGGCCCTCTTAGTGAAATGGCCCAATGATCTAGTTTCAAGATCTTGGAGGATGAA 480
Qy 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTrpTyrIleLeuAlaIleThr 180
Db 481 GGTAGT-----GAATGTGAACCTGGATTTTTCGGAATGGTACATCTTGGCATCACA 534
Qy 181 AlaPheLeuGluPheLeuLeuProValSerLeuValTyrPheSerValGlnIleTyr 200
Db 535 TCATCTTGGAAATTCGTGATCCCAAGTCACTCTTAGTCGCTTATTTCACATCAATATTAT 594
Qy 201 TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220
Db 595 TGGAGCCTGTGGAAGCGTGATCATCTCAGTAGGTGCCAAGCCATCTCGACTGCTGCT 654
Qy 221 ThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu 240
Db 655 GTCTCTTCCAACTCTGTGGACACTCATTTCAGAGGTAGACTATCTTCAAGAGATCTCTT 714
Qy 241 ProGlyLeuLysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSer 260
Db 715 TCTGCATCGACAGAAATTCCTGCATCTCTTCAVTCAGAGAGACAGAGAGAGAGTAGT 774
Qy 261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleLeuAlaPheLysValGlySer 280
Db 775 CTCATGTTTCTCAGAACCAAGATGAATAGCAATCAATTCCTCAAAATGGGTTC 834
Qy 281 PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300
Db 835 TTCTCCCAATCAGATCTGTAGCTCTTCCACCAAGGGAACATGTTGAACCTGTAGAGCC 894
Qy 301 ArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
Db 895 AGGAGATTAGCAAGTCACTGGCCATCTCTTAGGGGTTTGTGCTGTGCTGGCTCCA 954
Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle 340
Db 955 TATTCTCTGTTCACAAATGTCCTTTCATTTATTTCCTCAGCAACAGGTCTTAATCAGTT 1014
Qy 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnProPheLeuTyr 360
Db 1015 TGGTATAGAAATTCATTTGGCTCAGTGGTTCATTTCTTTTGTCAATCTCTTTTGAT 1074
Qy 361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysGln 380
Db 1075 CCATTGTGTCAAGCGCTTCAAAGGCTTCTTGAAGGCTTCTTGAATAATATTTGTATAAAGCAA 1134
Qy 381 ProAlaProSerGln---ThrGlnSerValSerSer 391
Db 1135 CCTTACCATCACAAACAGTCGGTCTAGTATCTTCT 1170
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RESULT 8

US-09-812-216-1

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; Sequence 1, Application US/09812216
; Patent No. US20020098539A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Jiang Xu
; APPLICANT: Hedrick, Joseph A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Monisma, Frederick J. Jr.
; APPLICANT: Morse, Kelley L.
; APPLICANT: Umland, Shelby P.
; APPLICANT: Wang, Suke
; TITLE OF INVENTION: Histamine receptor
; FILE REFERENCE: CN01069
; CURRENT APPLICATION NUMBER: US/09/812,216
; CURRENT FILING DATE: 2001-03-19
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; PRIOR APPLICATION NUMBER: 09/414,010
; PRIOR FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-812-216-1
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Alignment Scores:
Pred. No.: 5,7e-145 Length: 1173
Score: 1403.50 Matches: 271
Percent Similarity: 79.3% Conservative: 40
Best Local Similarity: 69.1% Mismatches: 78
Query Match: 68.6% Indels: 3
DB: 3 Gaps: 2
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US-10-626-126-9 (1-391) x US-09-812-216-1 (1-1173)

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Qy 1 MetSerGluSerAsnGlyThrAepValLeuProLeuThrAlaGlnValProLeuAlaPhe 20
Db 1 ATGCCAGATACTAATAGCACAATCAATTTATTCATCACTAAGCACTCGTGTACTTTAGCATTT 60
Qy 21 LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValValIleLeuAlaPhe 40
Db 61 TTTATGTCTTATAGCTTTTGTCTAATAGCTAGGAAATGCTTTGTTCATTTAGCTTTT 120
Qy 41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
Db 121 GTGGTGGACAAACCTTAGACATCGAAGTAGTATTATTTTCTTAACCTTGGCCATCTCT 180
Qy 61 AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTrp 80
Db 181 GACTTCTTGTGGGTGTGATCTCCATTCCTTTGTATCATCTCCACACGCTGTTCGAATGG 240
Qy 81 AsnProGlySerGlyIleCysMetPheTrpLeuIleThrAepTyrIleLeuLeuCysThrAla 100
Db 241 GATTTGGGAAGAAATCTGTGTATTGTGCTCAGTACTGACTATCTGTATGTACAGCA 300
Qy 101 SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
Db 301 TCTGTATATAACATTTGCTCTCATCAGTATGATCGATACCTGTGCTCAGTCTCAATGCTGTG 360
Qy 121 ArgTyrArgAlaGlnHisThrGlyIleLeuLysIleValAlaGlnMetValAlaValTTP 140
Db 361 TCTATAGAACTCAACATCTGGGCTCTGAAGATTGTTACTCTGATGGTGGCGTTGG 420
Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAepSerTrpLysAenSer 160
Db 421 GTGCTGGCCCTCTTAGTGAAATGGCCCAATGATCTTAGTTTCAGAGTCTTGGAGGATGAA 480
Qy 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTrpTyrIleLeuAlaIleThr 180
Db 481 GGTAGT-----GAATGTGAACCTGGATTTTTCGGAATGGTACATCTTGGCATCACA 534
Qy 181 AlaPheLeuGluPheLeuLeuProValSerLeuValTyrPheSerValGlnIleTyr 200
Db 535 TCATCTTGGAAATTCGTGATCCCAAGTCACTCTTAGTCGCTTATTTCACATCAATATTAT 594
Qy 201 TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220
Db 595 TGGAGCCTGTGGAAGCGTGATCATCTCAGTAGGTGCCAAGCCATCTCGACTGCTGCT 654
Qy 221 ThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu 240
Db 655 GTCTCTTCCAACTCTGTGGACACTCATTTCAGAGGTAGACTATCTTCAAGAGATCTCTT 714
Qy 241 ProGlyLeuLysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSer 260
Db 715 TCTGCATCGACAGAGTTCCTGCATCTCTTTCATTCAGAGAGACAGAGAGAGAGTAGT 774
Qy 261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleLeuAlaPheLysValGlySer 280
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Db 775 CTCAATGTTTCTCAAGAACCAAGATGAATAGCAATACAAATGCTTCCAAATGGGTTC 834
Qy 281 PheCysArgSerGluSerProValLeuHisGluArgGluHisValGluLeuLeuArgGly 300
Db 835 TTCTCCCAATCAATTCCTAGCTCTTCAACCAAGGGGAACATGTTGAACCTGTAGAGCC 894
Qy 301 ArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
Db 895 AGAGATAGCAAGTCACTGGCCATCTCTTAGGGGTTTTCGTGTTGCTGGGTCCA 954
Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle 340
Db 955 TATCTCTGTTCACAAATGCTCTTCAATTTATTCCTCAGCAACAGGTCTCAAAATCAGTT 1014
Qy 341 TrpTyrSerIleAlaPheThrLeuGlnTrpPheAsnSerLeuIleAsnProPheLeuTyr 360
Db 1015 TGGTATAGAAATTCGATTTTGGCTTCAGTGGTTCATTTCTTGTCAATCTCTTTGTAT 1074
Qy 361 ProLeuCysHisArgGluSerLeuValLeuLeuSerLeuIleAsnProPheLeuTyr 380
Db 1075 TGGTATAGAAATTCGATTTTGGCTTCAGTGGTTCATTTCTTGTCAATCTCTTTGTAT 1134
Qy 381 ProAlaProSerGln---ThrGlnSerValSerSer 391
Db 1135 CCTCTACCATCACACACAGTCGGTCAGTATCTTCT 1170

RESULT 9

US-09-910-411-1
; Sequence 1, Application US/09910411
; Patent No. US20020137054A1
; GENERAL INFORMATION:
; APPLICANT: Bergsma, Derek
; APPLICANT: Fitzgerald, Laura
; APPLICANT: Li, Xiatong
; APPLICANT: Michalovich, David
; APPLICANT: Zhu, Yuan
; TITLE OF INVENTION: AXOR35, A G-Protein Coupled Receptor
; FILE REFERENCE: GP70555-2C1
; CURRENT APPLICATION NUMBER: US/09/910,411
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 09/693,761
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/497,790
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/431,898
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-910-411-1

Alignment Scores:
Pred. No.: 5,76-145 Length: 1173
Score: 1403.50 Matches: 271
Percent Similarity: 79.3% Conservative: 40
Best Local Similarity: 69.1% Mismatches: 78
Query Match: 68.6% Indels: 3
DB: 2 Gaps: 2

US-10-626-126-9 (1-391) x US-09-910-411-1 (1-1173)

Qy 1 MetSerGluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe 20
Db 1 ATGCCAGATCAATAACCAATCAATTTATTCATCACTAAGCACTCGTGTACTTTAGCATTT 60
Qy 21 LeuMetSerLeuAlaPheAlaIleThrIleGlyAsnAlaValIleLeuAlaPhe 40
Db 61 TTTATGTCTCTTAGTAGCTTTTGTCTATTAATGCTAGGAAATGCTTTGGTTCATTTAGCTTTT 120

Qy 41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
Db 121 GTGGTGGACAAACCTTAGACATCAGATAGTATTATTTTCTTAACCTGGCACTCTCT 180
Qy 61 AppPheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTrp 80
Db 181 GACTTCTTGTGGGTGTGATCTCCATTCCTTTGTATCATCCCTCACACGCTGTTTGAATGG 240
Qy 81 AsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100
Db 241 GATTTTGGAAAGGAATCTGTGATTTTGGCTCACTACTGACTATCTGTATGTATACGCA 300
Qy 101 SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
Db 301 TCTGTATATAACATTCCTCATCTAGCTATGATCGATACCTGTGCTCAGTCTCAAAATGCTGTG 360
Qy 121 ArgTyrArgAlaGlnHisThrGlyIleLeuLysIleValAlaGlnMetValAlaValTrp 140
Db 361 TCTTATAGAACTCAACATCTGGGTCTTGAAGATTGTTACTCTGATGGTGGCCGTTTGG 420
Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160
Db 421 GTGCTGGCCTTCTTAGTGAATGGCCCAATGATTCATGTTTCAGAGTCTTGGAAAGGATGAA 480
Qy 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTrpTyrIleLeuAlaIleThr 180
Db 481 GGTAGT-----GAATGTGAACCTGGATTTTTCGGAATGGTACATCTCTGTCATCACA 534
Qy 181 AlaPheLeuGluPheLeuLeuProValSerLeuValValTyrPheSerValGlnIleTyr 200
Db 535 TCATTTCTTGGAAATTCGTATCCAGTCATCTTAGTCGCTTATTTCAACATGAATATTTAT 594
Qy 201 TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220
Db 595 TGGAGCCTGTGAAGCGTGATCATCTCAGTAGTGTCCAAAGCCATCTCTGGACGTGCT 654
Qy 221 ThrSerArgGlyThrGlyHisSerArgThrGlyLeuAlaCysArgThrSerLeu 240
Db 655 GTCTCTTCCAAACATCTGTGGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714
Qy 241 ProGlyLeuLysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSer 260
Db 715 TCTGCATCGACAGAACTTCTGTCATCTTTCATTCAGAGACAGAGGAGAAAGTAGT 774
Qy 261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleIleAlaPheLysValGlySer 280
Db 775 CTCATGTTTCTCAAGAACCAAGATGAATAGCAATACATTCATTCCTCCAAATGGGTTC 834
Qy 281 PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300
Db 835 TTCTCCCAATCAGATTCCTGTAGCTCTTCCAAAGGGGAACATGTTGAACCTGTAGAGCC 894
Qy 301 ArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
Db 895 AGAGATAGCAAGTCACTGGCCATCTCTTAGGGGTTTTCGTGTTGCTGGGTCCA 954
Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle 340
Db 955 TATCTCTGTTCACAAATGCTCTTCAATTTATTCCTCAGCAACAGGTCTCAAAATCAGTT 1014
Qy 341 TrpTyrSerIleAlaPheThrLeuGlnTrpPheAsnSerLeuIleAsnProPheLeuTyr 360
Db 1015 TGGTATAGAAATTCGATTTTGGCTTCAGTGGTTCATTTCTTGTCAATCTCTTTGTAT 1074
Qy 361 ProLeuCysHisArgGluSerLeuValLeuLeuSerLeuIleAsnProPheLeuTyr 380
Db 1075 CCATTTGTGCACAGCGCTTCAAAAGGCTTCTTGAANAATATTTGTATATAAAAGCA 1134
Qy 381 ProAlaProSerGln---ThrGlnSerValSerSer 391
Db 1135 CCTCTACCATCACACACAGTCGGTCAGTATCTTCT 1170

Db 1075 CCATTGTGTCAACAGCGCTTTCAAAAGGCTTCTTGAAATATTTTGTATATAAAAGCAA 1134
Qy 381 ProAlaProSerGln---ThrGlnSerValSerSer 391
Db 1135 CCTCTACCATCAACACACAGTCGGTCAGTATCTCT 1170
RESULT 11
US-09-876-252-13
; Sequence 13, Application US/09876252
; Publication No. US20030018182A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Lin, I-Lin
; APPLICANT: Dang, Huong T.
; APPLICANT: Chen, Ruoping
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: Non-Endogenous Constititively Activated Human G Protein Coupled Receptor
; FILE REFERENCE: AREN-0054
; CURRENT APPLICATION NUMBER: US/09/876,252
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 09/416,760
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/110,060
; PRIOR FILING DATE: 1998-11-27
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,852
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/123,944
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,945
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,948
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,951
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/152,524
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/151,114
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/108,029
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,127
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,131
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/141,448
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/156,555
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,634
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,653
; PRIOR FILING DATE: 1999-09-29

; PRIOR APPLICATION NUMBER: 60/157,280
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,294
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,281
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,282
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/156,633
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-876-252-13
Alignment Scores:
Pred. No.: 5,7e-145 Length: 1173
Score: 1403.50 Matches: 271
Percent Similarity: 79.3% Conservative: 40
Best Local Similarity: 69.1% Mismatches: 78
Query Match: 68.6% Indels: 3
DB: 3 Gaps: 2
US-10-626-126-9 (1-391) x US-09-876-252-13 (1-1173)
Qy 1 MetSerGluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe 20
Db 1 ATGCCAGATACATAATAGCACAAATCAATTTATCATAAGCACTCGTGTACTTTAGCATTT 60
Qy 21 LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValValIleLeuAlaPhe 40
Db 61 TTTATGTCTTGTAGTCTTTTGTCTAATAGTAGGAAATGCTTTGTGCTATTTAGCTTTT 120
Qy 41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
Db 121 GTGGTGGACAAAACCTTAGACATCGAAGTAGTATTATTTTCTTAACCTTGGCATCTCT 180
Qy 61 AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTyr 80
Db 181 GACTTCTTTGTGGTGTGATCTCCATTCCTTTGTATACATCCCTCACACGCTGTCGAATGG 240
Qy 81 AsnProGlySerGlyIleCysMetPheTyrLeuIleThrAspTyrLeuLeuCysThrAla 100
Db 241 GATTTTGGAAAGGAAATCTGTGATTTTGGCTCACTACTACTACTATCTGTATGTAGCAGCA 300
Qy 101 SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
Db 301 TCTGTATATACATTTCTCTCATCAGCTATGATCGATACCTGTCACTCTCAATGTGTGG 360
Qy 121 ArgTyrArgAlaGlnHisThrGlyIleLeuLysIleValAlaGlnMetValAlaValTyr 140
Db 361 TCTTATAGAACTCAACATACATCGGGCTTGAAGATTGTTACTCTGTATGCGCGTGTGG 420
Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTyrIleAsnSer 160
Db 421 GTGCTGGCCCTTCTTAGTGAATGGGCAATGATTTAGTTTTCAGAGTCTTGGAGGATGAA 480
Qy 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTyrTyrIleLeuAlaIleThr 180
Db 481 GGTAGT-----GATGTGAACCTGGATTTTTCGGAATGGTACATCTTGGCATCACA 534
Qy 181 AlaPheLeuGluPheLeuLeuProValSerLeuValValTyrPheSerValGlnIleTyr 200
Db 535 TCATCTTGGAAATTCGTGATCCAGTCATCTTAGTCGCTATTATTCAACATGAATATTAT 594
Qy 201 TrpSerLeuTyrIleArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220
Db 595 TGGAGCCTGTGGAAGCGTGCATCATCTCAGTAGGTGCAAGGCCATCTCGACTGACTGTCT 654
Qy 221 ThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu 240


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Db 715 TCTGCATCGACAGAGAGTTCCTGCATCTCTTCATTCAGAGAGACAGAGAGAGTAGT 774
Qy 261 LeuLeuValSerLeuArgThrHisMetSerGlySerLeuLeuAlaPheLysValGlySer 280
Db 775 CTCTATGTTTCTCAAGAACCAAGATGAATAGCAATACAATTCCTCAAAATGGGTTC 834
Qy 281 PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300
Db 835 TTCTCCCATCGAATCTGTAGCTCTTCACCAAGGGACATGTTGAACCTGTAGAGCC 894
Qy 301 ArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaLeuCysTrpAlaPro 320
Db 895 AGGAGATTAGCAAGTCACTGGCCATCTCTTAGGGGGTTTTGCTGTGGCTCCA 954
Qy 321 TyrCysLeuPheThrLeuValLeuSerThrTyrArgArgGlyGluArgProLysSerIle 340
Db 955 TATTCTCTGTTTCAAAATGTCTTTTCATTTTATTCCTCAGCAACAGGTCTCTAAATCAGT 1014
Qy 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnProPheLeuTyr 360
Db 1015 TGGTATAGAAATGCAATTTGGCTTCAGTGGTTCATTTCTTTGCAATCTCTTTTGTAT 1074
Qy 361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysGln 380
Db 1075 CCATTGTGTACAGCGCTTCAAAAGCGCTTCTTGAATAATATTTGTATAAAAGCAA 1134
Qy 381 ProAlaProSerGln---ThrGlnSerValSerSer 391
Db 1135 CCTTACCATCACACACAGTCGGTCAAGTATCTTCT 1170
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RESULT 12

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US-10-052-193-1
; Sequence 1, Application US/10052193
; Publication No. US20020132755A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer, Inc.
; TITLE OF INVENTION: HISTAMINE RECEPTOR ANTAGONISTS
; FILE REFERENCE: PC10963A
; CURRENT APPLICATION NUMBER: US/10/052.193
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 0101223.6
; PRIOR FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-052-193-1
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Alignment Scores:
Pred. No.: 5.7e-145 Length: 1173
Score: 1403.50 Matches: 271
Percent Similarity: 79.3% Conservative: 40
Best Local Similarity: 69.1% Mismatches: 78
Query Match: 68.6% Indels: 3
DB: 5 Gaps: 2
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US-10-626-126-9 (1-391) x US-10-052-193-1 (1-1173)

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Qy 1 MetSerGluSerAsnArgThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe 20
Db 1 ATGCCAGATACTAATAGCACAAATCAATTTATCACTAAAGCATCGTGTACTTTAGCAATTT 60
Qy 21 LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValAlaLeuAlaPhe 40
Db 61 TTTATGTCCTTAGTAGCTTTTGTATATGCTAGGAATGCTTTTGGTCAATTTTAGCTTTT 120
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RESULT 13

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Qy 41 ValAlaAspArgGlnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
Db 121 GTGTGTGACAAACCTTAGACATCGAAGTAGTATATTTTCTTAACCTTGGCCATCTCT 180
Qy 61 AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTrp 80
Db 181 GACTCTTTTGGGTGTGATCTCCATTCCTTTGTATCATCCCTCACACGCTGTTCGAATGG 240
Qy 81 AsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100
Db 241 GATTTTGGAAGGAATCTGTGTATTTTGGCTACTACTGACTATCTGTATGTATGACAGCA 300
Qy 101 SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
Db 301 TCTGTATATACATTTGCTCCTCATCAGTATGATCGATACCTGTCAAGTCTCAATATGCTGTG 360
Qy 121 ArgTyrArgAlaGlnHisThrGlyIleLeuLysIleValAlaGlnMetValAlaValTrp 140
Db 361 TCTATAGAACTCAACATACCTGGGGTCTTGAAGATTGTACTCTGTATGGTGGCGTTTGG 420
Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160
Db 421 GTGCTGGCCCTTCTTAGTGAATGGGCCAATGATTCTAGTTTCAGAGTCTTGGGAAGATGAA 480
Qy 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTrpTyrIleLeuAlaIleThr 180
Db 481 GGTAGT-----GAATGTGAACCTGGAAATTTTTCGGAATGGTACATCTCTTGGCCATACA 534
Qy 181 AlaPheLeuGluPheLeuLeuProValSerLeuValValTyrPheSerValGlnIleTyr 200
Db 535 TCATTTCTGGAAATTCGTGATCCCGATCATCTTAGTCGCTTATTTCAACATGAATATTAT 594
Qy 201 TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220
Db 595 TGGAGCCTGTGGAAGCGTGATCATCTCAGTAGGTGSCAAAGCCATCTCTGGACTGACTGCT 654
Qy 221 ThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu 240
Db 655 GTCTCTTCCAAACATCTGTGACACTCAATTCAGAGGTAGACTATCTTCAGAGAGATCTCT 714
Qy 241 ProGlyLeuLysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSer 260
Db 715 TCTGCATCGACAGAGTTCCTGCATCTCTTTCATTCAGAGAGACAGAGAGAGTAGT 774
Qy 261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleLeuAlaPheLysValGlySer 280
Db 775 CTCAATGTTTCTCAGAGAACCAAGATCAATAGCAATACAATTCCTTCCAAATGGGTTC 834
Qy 281 PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300
Db 835 TTCTCCCAATCAGATTCTGTAGCTCTTTCACCAAGGGAACATGTTGAACCTCTTAGAGCC 894
Qy 301 ArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
Db 895 AGGAGATTAGCAAGTCACTGGCCATCTCTTAGGGGGTTTTGCTGTGTGGCTCCA 954
Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle 340
Db 955 TATTCTCTGTTTCAAAATGTCTTTTCATTTTATTCCTCAGCAACAGGTCTCTAAATCAGT 1014
Qy 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnProPheLeuTyr 360
Db 1015 TGGTATAGAAATGCAATTTGGCTTCAGTGGTTCATTTCTTTGCAATCTCTTTTGTAT 1074
Qy 361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysGln 380
Db 1075 CCATTGTGTACAGCGCTTCAAAAGCGCTTCTTGAATAATATTTGTATAAAAGCAA 1134
Qy 381 ProAlaProSerGln---ThrGlnSerValSerSer 391
Db 1135 CCTTACCATCACACACAGTCGGTCAAGTATCTTCT 1170
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US-10-272-983-13		US-10-626-126-9 (1-391) x US-10-272-983-13 (1-1173)	
; Sequence 13, Application US/10272983		Qy 1 MetSerGluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe 20	
; Publication No. US20030148450A1		Db 1 ATGCAGATACCTAATAGCAATCAATTTATCACTAAGCACTCGTGTACTTTAGCATTT 60	
; GENERAL INFORMATION:		Qy 21 LeuMetSerLeuAlaPheAlaThrIleGlyAsnAlaValValIleLeuAlaPhe 40	
; APPLICANT: Chen, Ruoping		Db 61 TTTATGTCCTTAGAGCTTTGTCTAATCTAGGAATGCTTTGTCTATTTAGCTTTT 120	
; APPLICANT: Dang, Huong T.		Qy 41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60	
; APPLICANT: Liaw, Chen W.		Db 121 GTGTGGACAAAACCTTAGCATCGAAGTAGTATTTTCTTAACTTGGCCATCTCT 180	
; APPLICANT: Lin, I-Lin		Qy 61 AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTyr 80	
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors		Db 181 GACTTCTTTGGGTGTGATCTCCATTCCTTTGTACATCCCTCACAGCTGTTTGAATGG 240	
; FILE REFERENCE: AREN0050		Qy 81 AsnProGlySerGlyIleCysMetPheThrLeuIleThrAspTyrLeuLeuCysThrAla 100	
; CURRENT APPLICATION NUMBER: US/10/272,983		Db 241 GATTTTGGAAAGGAATCTGTGATTTTGGCTCACTACTGACTATCTGTTATGTACAGCA 300	
; CURRENT FILING DATE: 2002-10-17		Qy 101 SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120	
; PRIOR APPLICATION NUMBER: US/09/417,044			
; PRIOR FILING DATE: 1999-10-12			
; PRIOR APPLICATION NUMBER: 60/109,213			
; PRIOR FILING DATE: 1998-11-20			
; PRIOR APPLICATION NUMBER: 60/120,416			
; PRIOR FILING DATE: 1999-02-16			
; PRIOR APPLICATION NUMBER: 60/121,851			
; PRIOR FILING DATE: 1999-02-26			
; PRIOR APPLICATION NUMBER: 60/123,946			
; PRIOR FILING DATE: 1999-03-12			
; PRIOR APPLICATION NUMBER: 60/123,949			
; PRIOR FILING DATE: 1999-03-12			
; PRIOR APPLICATION NUMBER: 60/136,436			
; PRIOR FILING DATE: 1999-05-28			
; PRIOR APPLICATION NUMBER: 60/136,437			
; PRIOR FILING DATE: 1999-05-28			
; PRIOR APPLICATION NUMBER: 60/136,439			
; PRIOR FILING DATE: 1999-05-28			
; PRIOR APPLICATION NUMBER: 60/136,567			
; PRIOR FILING DATE: 1999-05-28			
; Remaining Prior Application data removed - See File Wrapper or PALM.			
; NUMBER OF SEQ ID NOS: 74			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 13			
; LENGTH: 1173			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-10-272-983-13			
Alignment Scores:			
Pred. No.:	5.7e-145	Length:	1173
Score:	1403.50	Matches:	271
Percent Similarity:	79.3%	Conservative:	40
Best Local Similarity:	69.1%	Mismatches:	78
Query Match:	68.6%	Indels:	3
DB:	6	Gaps:	2
US-10-626-126-9 (1-391) x US-10-272-983-13 (1-1173)			
Qy 1 MetSerGluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe 20			
Db 1 ATGCAGATACCTAATAGCAATCAATTTATCACTAAGCACTCGTGTACTTTAGCATTT 60			
Qy 21 LeuMetSerLeuAlaPheAlaThrIleGlyAsnAlaValValIleLeuAlaPhe 40			
Db 61 TTTATGTCCTTAGAGCTTTGTCTAATCTAGGAATGCTTTGTCTATTTAGCTTTT 120			
Qy 41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60			
Db 121 GTGTGGACAAAACCTTAGCATCGAAGTAGTATTTTCTTAACTTGGCCATCTCT 180			
Qy 61 AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTyr 80			
Db 181 GACTTCTTTGGGTGTGATCTCCATTCCTTTGTACATCCCTCACAGCTGTTTGAATGG 240			
Qy 81 AsnProGlySerGlyIleCysMetPheThrLeuIleThrAspTyrLeuLeuCysThrAla 100			
Db 241 GATTTTGGAAAGGAATCTGTGATTTTGGCTCACTACTGACTATCTGTTATGTACAGCA 300			
Qy 101 SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120			

US-10-354-769-1
; Sequence 1, Application US/10354769
; Publication No. US20030149242A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: O'Reilly, Mark A.
; APPLICANT: Peter, Beate
; TITLE OF INVENTION: NOVEL POLYPEPTIDE
; FILE REFERENCE: PC10373B
; CURRENT APPLICATION NUMBER: US/10/354,769
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 09/698,801
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/211,243

RESULT 14

; PRIOR FILING DATE: 2000-06-14
 ; PRIOR APPLICATION NUMBER: GB 9925641.4
 ; PRIOR FILING DATE: 1999-10-29
 ; PRIOR APPLICATION NUMBER: GB 0009973.9
 ; PRIOR FILING DATE: 2000-04-20
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1
 ; LENGTH: 1173
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-354-769-1

Alignment Scores:
 Pred. No.: 5,7e-145 Length: 1173
 Score: 1403.50 Matches: 271
 Percent Similarity: 79.3% Conservative: 40
 Best Local Similarity: 69.1% Mismatches: 78
 Query Match: 68.6% Indels: 3
 DB: Gaps: 2

US-10-626-126-9 (1-391) x US-10-354-769-1 (1-1173)

Qy	1	MetSerGluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe	20
Db	1	ATGCCAGATACATAATAGCAACATCAATTTATCACTAAGCACCTCGTGTACTTTAGCATTT	60
Qy	21	LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValIleLeuAlaPhe	40
Db	61	TTTATGTCTTAGTACTTTTGTATTAAGCTAGGAAATGCTTTGGTCAATTTAGCTTTT	120
Qy	41	ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer	60
Db	121	GTGGTGACAAACCTTAGACATCGAAGTAGTTATTTTCTTAACTTTGGCCATCTCT	180
Qy	61	AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrIleuPheAsnTrp	80
Db	181	GACTTCTTTGTGGGTGTGATCTCCATTCCTTTGTATCATCCCTCACACGCTGTTCGAATGG	240
Qy	81	AsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla	100
Db	241	GATTTTGGAAAGGAATCTGTGTATTTTGGCTCACTAGCTACTCTGTATGTACAGCA	300
Qy	101	SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal	120
Db	301	TCGTATATAACATCTCTCATCAGCTATGATCGATACCTGTCACTGCTCAAAATGCTGTG	360
Qy	121	ArgTyrArgAlaGlnHisThrGlyIleLeuIleValIleAlaGlnMetValAlaValTrp	140
Db	361	TCATTATAGAACTCAACATACCTGGGGTCTTGAAGATTTGTTACTCTGATGGTGGCCGCTTGG	420
Qy	141	IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpIleAsnSer	160
Db	421	GTGCTGGCTCTCTTAGTGAATGGGCCAAGATTTAGTTTTCAGAGCTTTGGAAGATGAA	480
Qy	161	ThrAsnThrGluGluCysGluProGlyPheValThrGluTrpTyrIleLeuAlaIleThr	180
Db	481	GGTAGT-----GAATGTGAACCTGGATTTTTCGGAATGGTACATCTTTGCCATCACA	534
Qy	181	AlaPheLeuGluPheLeuProValSerLeuValValTyrPheSerValGlnIleTyr	200
Db	535	TCATTCTTGGAAATTCGTGATCCAGTCATCTTAGTCGCTTAATTTCAACATGAATATTTAT	594
Qy	201	TrpSerLeuTrpIleArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla	220
Db	595	TGGAGCTGTGGGAAGCGGTGATCATCTCAGTAGGTGCCAAAGCCATCTCGAGCTGCTGCT	654
Qy	221	ThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu	240
Db	655	GTCTCTTCCAAACATCTGTGGACACTCATTCAGAGGTAGTACTATCTTCAGGAGATCTCTT	714
Qy	241	ProGlyLeuIleGluProAlaAlaSerLeuHisSerGluSerProArgGlyIleSerSer	260

; PRIOR FILING DATE: 2000-06-14
 ; PRIOR APPLICATION NUMBER: GB 9925641.4
 ; PRIOR FILING DATE: 1999-10-29
 ; PRIOR APPLICATION NUMBER: GB 0009973.9
 ; PRIOR FILING DATE: 2000-04-20
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1
 ; LENGTH: 1173
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-354-769-1

Alignment Scores:
 Pred. No.: 5,7e-145 Length: 1173
 Score: 1403.50 Matches: 271
 Percent Similarity: 79.3% Conservative: 40
 Best Local Similarity: 69.1% Mismatches: 78
 Query Match: 68.6% Indels: 3
 DB: Gaps: 2

US-10-626-126-9 (1-391) x US-10-354-769-1 (1-1173)

Qy	1	MetSerGluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe	20
Db	1	ATGCCAGATACATAATAGCAACATCAATTTATCACTAAGCACCTCGTGTACTTTAGCATTT	60
Qy	21	LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValIleLeuAlaPhe	40
Db	61	TTTATGTCTTAGTACTTTTGTATTAAGCTAGGAAATGCTTTGGTCAATTTAGCTTTT	120
Qy	41	ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer	60
Db	121	GTGGTGACAAACCTTAGACATCGAAGTAGTTATTTTCTTAACTTTGGCCATCTCT	180
Qy	61	AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrIleuPheAsnTrp	80
Db	181	GACTTCTTTGTGGGTGTGATCTCCATTCCTTTGTATCATCCCTCACACGCTGTTCGAATGG	240
Qy	81	AsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla	100
Db	241	GATTTTGGAAAGGAATCTGTGTATTTTGGCTCACTAGCTACTCTGTATGTACAGCA	300
Qy	101	SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal	120
Db	301	TCGTATATAACATCTCTCATCAGCTATGATCGATACCTGTCACTGCTCAAAATGCTGTG	360
Qy	121	ArgTyrArgAlaGlnHisThrGlyIleLeuIleValIleAlaGlnMetValAlaValTrp	140
Db	361	TCATTATAGAACTCAACATACCTGGGGTCTTGAAGATTTGTTACTCTGATGGTGGCCGCTTGG	420
Qy	141	IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpIleAsnSer	160
Db	421	GTGCTGGCTCTCTTAGTGAATGGGCCAAGATTTAGTTTTCAGAGCTTTGGAAGATGAA	480
Qy	161	ThrAsnThrGluGluCysGluProGlyPheValThrGluTrpTyrIleLeuAlaIleThr	180
Db	481	GGTAGT-----GAATGTGAACCTGGATTTTTCGGAATGGTACATCTTTGCCATCACA	534
Qy	181	AlaPheLeuGluPheLeuProValSerLeuValValTyrPheSerValGlnIleTyr	200
Db	535	TCATTCTTGGAAATTCGTGATCCAGTCATCTTAGTCGCTTAATTTCAACATGAATATTTAT	594
Qy	201	TrpSerLeuTrpIleArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla	220
Db	595	TGGAGCTGTGGGAAGCGGTGATCATCTCAGTAGGTGCCAAAGCCATCTCGAGCTGCTGCT	654
Qy	221	ThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu	240
Db	655	GTCTCTTCCAAACATCTGTGGACACTCATTCAGAGGTAGTACTATCTTCAGGAGATCTCTT	714
Qy	241	ProGlyLeuIleGluProAlaAlaSerLeuHisSerGluSerProArgGlyIleSerSer	260

; PRIOR FILING DATE: 2000-06-14
 ; PRIOR APPLICATION NUMBER: GB 9925641.4
 ; PRIOR FILING DATE: 1999-10-

Pred. No.: 5,7e-145 Length: 1173
Score: 1403.50 Matches: 271
Percent Similarity: 79.3% Conservative: 40
Best Local Similarity: 69.1% Mismatches: 78
Query Match: 68.6% Indels: 3
DB: 2

US-10-626-126-9 (1-391) x US-10-393-807-13 (1-1173)

QY 1 MetSerGluSerArgGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe 20
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 1 ATGCCAGATACTAATAGCACAAATTTATCACTAAGCACTCGTGTTACTTTAGCATTT 60
QY 21 LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValValIleLeuAlaPhe 40
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 61 TTTATGTCCTTAGTAGCTTTGCTATTAATCTAGGAAATGCTTTGGTTCATTTTAGCTTTT 120
QY 41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 121 GTGTGGGACAAAACCTTACACATCGAAGTAGTTATTTTTTTCTTAACTTGGCCATCTCT 180
QY 61 AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTyr 80
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 181 GACTTCTTTGTGGGTGTGATCTCCATTCCTTTGTACATCCCTCACACGCTGTTCGAATGG 240
QY 81 AsnProGlySerGlyIleCysMetPheTyrLeuIleThrAspTyrLeuLeuCysThrAla 100
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 241 GATTTGGAAAGGAATCTGTGTATTTTGGCTCACTACTGACTATCTGTTATGTACAGCA 300
QY 101 SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 301 TCTGTATATAACATTTGCTCTCATCGCTATGATCGATACCTGTGCTCAATGCTGTG 360
QY 121 ArgTyrArgAlaGlnHisThrGlyIleLeuIleValIleValAlaGlnMetValAlaValTyr 140
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 361 TCTATTAGAACTCAACATCTGGGGTCTTGAAGATTGTACTCTGATGGTGGCCGTTTGG 420
QY 141 IleLeuAlaPheLeuValAlaGlnGlyProMetIleLeuAlaSerAspSerTyrLysAsnSer 160
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Db 421 GTCTGGCCCTCTTAGTGAATGGCCATGATTTCTAGTTTCAGAGTCTTGGAAAGGATGAA 480
QY 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTyrTyrIleLeuAlaIleThr 180
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 481 GGTAGT-----GAATGTGAACCTGGATTTTTTTCGGAATGGTACATCTCTGCCATCACA 534
QY 181 AlaPheLeuGluPheLeuProValSerLeuValValTyrPheSerValGlnIleTyr 200
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Db 535 TCATTTCTGGAAATTCGTGATCCCGATCTCTTAGTCGCTTATTTCAACATGAATATTTAT 594
QY 201 TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 595 TGGAGCCTGTGGAGGGGTGATCATCTCAGTAGGTGCCAAGCCATCTCTGACCTGACTGCT 654
QY 221 ThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu 240
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Db 655 GTCTCTTCCAACATCTGTGGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714
QY 241 ProGlyLeuLysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSer 260
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Db 715 TCTGCATCCGACAGAAGTTCTCGCATCTCTTTCAVTCAGAGACAGAGGAGAAAGTAGT 774
QY 261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleIleAlaPheLysValGlySer 280
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 775 CTCAATTTTCTCAAGAACCAAGATGAATAGCAATGCTTCCAAAATGGGTTC 834
QY 281 PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 835 TTCTCCCAATCAGATCTGTAGCTCTTCCACAAAAGGGAAACATGTGTAACCTGTCTAGAGCC 894
QY 301 ArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysThrAlaPro 320
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 895 AGGAGATTAGCCAAGTCACTGGCCATTTCTCTTAGGGGGTTTTTGTGTTGCTGGCTCCA 954

Search completed: April 29, 2006, 02:16:03
Job time : 882 secs

QY 321 TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle 340
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 955 TATTCTCTGTTCACAATTTGCTTTTCATTTTATTCCTCAGCAACAGGTCCTAAATCAGTT 1014
QY 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnProPheLeuTyr 360
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 1015 TGGTATAGAAATTCGCAATTTTGGCTTCAGTGGTTCGAATTCCTTTGTCAATCCTCTTTGTAT 1074
QY 361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysGln 380
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 1075 CCATTGTGTACACAGGCGCTTCAAAAGGCTTCTTGAAAATATTTTGTATATAAAAGCAA 1134
QY 381 ProAlaProSerGln---ThrGlnSerValSerSer 391
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Db 1135 CCTTACCATCAACACACAGTCGGTCAGTATCTTCT 1170

GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 29, 2006, 02:01:23 ; Search time 5383 Seconds
(without alignments)
294.995 Million cell updates/sec

Title: US-10-626-126-9

Perfect score: 2045

Sequence: 1 MSESNGTDVLPTRAQVPLA.....WKILCVTKQAPAPSGTQSVSS 391

Scoring table:

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Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Dgapop 6.0 , Delext 7.0	

Searched: 9295968 seqs, 2030634719 residues

Total number of hits satisfying chosen parameters: 18591936

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlp
-Q=/abs/ABSSWEB.spool/US10626126/runat 25042006 180042 19317/app_query.fasta 1
-DB=Published Applications NA New -QFMT=fastap -SURFIX=p2n.rnpbn -MINMATCH=0.1
-LOOPCL=0 -LOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blsum62
-TRANS=human40.cdi -LIST=45 -DALIGN=200 -THR_SCORE=pet -THR_MAX=100
-MAXLEN=2000000000 -HOST=abs03p
-USER=US10626126 @CGN 1.1 994 @runat 25042006 180042 19317 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THRAUS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOF=6 -FGAPEXT=7
-YGAPOF=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA New:

1:	/SID55/ptodata/2/pubpna/US08 NEW PUB seq.*
2:	/SID55/ptodata/2/pubpna/US06 NEW PUB seq.*
3:	/SID55/ptodata/2/pubpna/US07 NEW PUB seq.*
4:	/SID55/ptodata/2/pubpna/PCT NEW PUB seq.*
5:	/SID55/ptodata/2/pubpna/US09 NEW PUB seq.*
6:	/SID55/ptodata/2/pubpna/US09 NEW PUB seq.*
7:	/SID55/ptodata/2/pubpna/US10 NEW PUB seq.*
8:	/SID55/ptodata/2/pubpna/US10 NEW PUB seq.*
9:	/SID55/ptodata/2/pubpna/US10 NEW PUB seq.*
10:	/SID55/ptodata/2/pubpna/US10 NEW PUB seq.*
11:	/SID55/ptodata/2/pubpna/US11 NEW PUB seq.*
12:	/SID55/ptodata/2/pubpna/US11 NEW PUB seq.*
13:	/SID55/ptodata/2/pubpna/US11 NEW PUB seq.*
14:	/SID55/ptodata/2/pubpna/US11 NEW PUB seq.*
15:	/SID55/ptodata/2/pubpna/US60 NEW PUB seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	682	33.3	2761	11	US-11-036-196-2003 Sequence 2003, Ap
2	682	33.3	2814	14	US-11-136-527-3990 Sequence 3990, Ap

3	621	30.4	2824	14	US-11-136-527-127	Sequence 127, Ap
4	594	29.0	1326	14	US-11-241-956-19	Sequence 19, Appl
5	407.5	19.9	2348	14	US-11-136-527-3691	Sequence 3691, Ap
6	405	19.8	1773	14	US-11-127-877-17	Sequence 17, Appl
7	405	19.8	1974	14	US-11-124-368A-14	Sequence 14, Appl
8	401	19.6	2733	14	US-11-136-527-2435	Sequence 2435, Ap
9	400.5	19.6	4095	14	US-11-136-527-2030	Sequence 2030, Ap
10	400	19.6	2699	14	US-11-127-877-5	Sequence 5, Appl
11	399.5	19.5	3578	11	US-11-036-196-1495	Sequence 1495, Ap
12	392	19.2	2633	14	US-11-136-527-3114	Sequence 3114, Ap
13	387.5	18.9	1860	14	US-11-136-527-2642	Sequence 2642, Ap
14	376.5	18.4	3741	14	US-11-136-527-751	Sequence 751, App
15	374.5	18.3	4061	14	US-11-136-527-2806	Sequence 2806, Ap
16	372.5	18.2	2089	14	US-11-128-061-892	Sequence 892, App
17	372.5	18.2	2089	14	US-11-128-049-892	Sequence 892, App
18	370.5	18.1	1303	14	US-11-128-061-570	Sequence 570, App
19	370.5	18.1	1303	14	US-11-128-049-570	Sequence 570, App
20	365.5	17.9	2089	14	US-11-127-877-14	Sequence 14, Appl
21	365.5	17.9	2290	14	US-11-127-877-13	Sequence 13, Appl
22	361	17.7	1401	14	US-11-127-877-4	Sequence 4, Appl
23	359	17.6	85980	11	US-11-114-798-46	Sequence 46, Appl
24	359	17.6	197241	11	US-11-114-798-47	Sequence 47, Appl
25	357.5	17.5	1496	14	US-11-136-527-2608	Sequence 2608, Ap
26	356.5	17.4	1443	8	US-10-521-162-39	Sequence 39, Appl
27	356.5	17.4	1443	8	US-10-521-162-41	Sequence 41, Appl
28	353	17.3	2591	14	US-11-136-527-1944	Sequence 1944, Ap
29	352.5	17.2	1203	9	US-10-499-210-1	Sequence 1, Appl
30	349.5	17.1	2483	14	US-11-136-527-2847	Sequence 2847, Ap
31	349.5	17.1	2509	14	US-11-136-527-3738	Sequence 3738, Ap
32	341.5	16.7	1435	8	US-10-750-185-26145	Sequence 26145, A
33	341.5	16.7	1435	8	US-10-750-623-26145	Sequence 26145, A
34	339.5	16.6	3893	14	US-11-136-527-2295	Sequence 2295, Ap
35	337.5	16.5	1350	11	US-11-232-805-24	Sequence 24, Appl
36	337.5	16.5	1862	14	US-11-136-527-2377	Sequence 2377, Ap
37	337.5	16.5	2809	14	US-11-136-527-2036	Sequence 2036, Ap
38	336.5	16.5	1350	11	US-11-232-805-25	Sequence 25, Appl
39	333.5	16.3	1552	14	US-11-136-527-2107	Sequence 2107, Ap
40	329	16.1	1344	11	US-11-232-805-2	Sequence 2, Appl
41	328.5	16.1	1353	11	US-11-232-805-1	Sequence 1, Appl
42	328.5	16.1	6501	14	US-11-136-527-3427	Sequence 3427, Ap
43	315.5	15.4	1269	14	US-11-136-527-3749	Sequence 3749, Ap
44	311.5	15.2	5616	14	US-11-136-527-2020	Sequence 2020, Ap
45	303	14.8	6244	14	US-11-136-527-3243	Sequence 3243, Ap

ALIGNMENTS

RESULT 1
US-11-036-196-2003
; Sequence 2003, Application US/11036196
; Publication No. US20060078900A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Higgins, Brandon
; APPLICANT: Castle, Arthur
; APPLICANT: Elashoff, Michael
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5089-US
; CURRENT APPLICATION NUMBER: US/11/036,196
; CURRENT FILING DATE: 2005-01-18
; PRIOR APPLICATION NUMBER: US/10/152,319
; PRIOR FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: US 60/292,335
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/297,523
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,925
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,810
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/303,807

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; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/303,808
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/315,047
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: US 60/324,928
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US 60/330,867
; PRIOR FILING DATE: 2001-11-01
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2221
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2003
; LENGTH: 2761
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. NM_053506
US-11-036-196-2003

Alignment Scores:
Pred. No.: 1.19e-50 Length: 2761
Score: 682.00 Matches: 160
Percent Similarity: 48.8% Conservative: 51
Best Local Similarity: 37.0% Mismatches: 133
Query Match: 33.3% Indels: 88
DB: 11 Gaps: 10

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Qy 38 LeuAlaPheValAlaPheArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeu 57
Db 506 CTGGCTTCGTGGCGATTCCAGCTCCGCCACCACTTCTTTCTGCTCAACCTC 565
Qy 58 AlaIleSerAspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeu 77
Db 566 GCATCTCCGACTTCTCTGGGGTGGCTTCTGATCCCATGTCAGTACCCCTATGTCG 625
Qy 78 Phe---AsnTrpAsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeu 96
Db 626 ACCGGCGGTGGACCTTCGGCGGGGCTCTGCAAGCTGGCTGGTGGTAGACTACTA 685
Qy 97 LeuCysThrAlaSerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerVal 116
Db 686 CTGTGTGCTTCTCGGTCTTCAACATCGTACTCATCAGTATGACCGATTCTGTGAGTC 745
Qy 117 SerAsnAlaValArgTyrArgAlaGlnHisThrGlyIleLeuIleValAlaGlnMet 136
Db 746 ACTCGAGCTGTCTTACAGGGGCCACAGGGGACACAGAGAGCGGGCGGTTCGGAAGTG 805
Qy 137 ValAlaValTrpIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSer 156
Db 806 GCATGTGTGGTGTGGCTTCTCTGCTATGGGCTGCCATCTG-----AGT 856
Qy 157 TrpLys-----AsnSerThrAsnThrGluGluCysGluProGlyPheVal 171
Db 857 TGGGAGTACCTGTGTGGTGCAGTTCCATCCCGAGGGCCACTGCTATGCTGAGTTCTTC 916
Qy 172 ThrGluTrpTrpIleLeuAlaIleThrAlaPheLeuGluPheLeuProValSerLeu 191
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Qy 192 ValValTyrPheSerValGlnIleTyr----- 200
Db 977 GTTACCTTCTTCAACCTCAGCATCTACTGAACATCCAGAGCGCACCGCGCTTCGGCTT 1036
Qy 200 ----- 200
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Db 1097 GCTCCCCCAGCTGCTGGGGCTGCTGGCCAAAGGCGCATGGCGAGCCATGCCGTTGCAC 1156
Qy 216 AlaGlyPheIleAlaThrSerSerArgGlyThr-----Gly 227
Db 1157 AGGTATGGGTGGTGGTGGAGCGCCCTGGTGTGTAGGCTGGGAGGCTGCCCTCGGGGT 1216
Qy 228 HisSerArgArgThrGlyLeuAlaCysArgThrSerLeuProGlyLeuLysGluProAla 247
Db 1217 GGCAGTGGTGGAGGTGCTGCTCGCCACCTCCAGCTCTGGC-----AGC 1264
Qy 248 AlaSerLeuHisSerGluSerProArgGlyLysSerSerLeuLeuValSerLeuArgThr 267
Db 1265 TCCTCAAGGGGCACTGAGGGCCACGC----- 1291
Qy 268 HisMetSerGlySerIleIleAlaPheLysValGlySerPheCysArgSerGluSerPro 287
Db 1292 -----TCACTCAAAAGGGGCTCCAAAGCATCAGCATCTTCAGCA 1330
Qy 288 ValLeuHisGlnArg-----GluHisValGluLeuLeu 298
Db 1331 TCCTTGGAGAAGGCGCATGAAGTGTCTCCAGAGCATCACCGCGCTTCCGGCTGTCG 1390
Qy 299 ArgGlyArgLysLeuAlaArgSerLeuAlaValLeuSerAlaPheAlaIleCysTrp 318
Db 1391 CGGACACAGAGGTGGCCAAAGTCTGCTGGCCATCATCGTGGAGCATCTTGGGCTCTGCTG 1450
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Db 1451 GCGCCGTACACGCTCTCTAATGATCATCCGAGCTGTTCG---CATGGCCGCTGCATCCCC 1507
Qy 339 SerIleTrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnProPhe 358
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RESULT 2
US-11-136-527-3990
; Sequence 3990, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3990
; LENGTH: 2814
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-3990

Alignment Scores:
Pred. No.: 1.22e-50 Length: 2814
Score: 682.00 Matches: 160
Percent Similarity: 48.8% Conservative: 51
Best Local Similarity: 37.0% Mismatches: 133
Query Match: 33.3% Indels: 88
DB: 14 Gaps: 10
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Db 496 CTCGCTTCGTGGCGGATTCGAGGCTCCGACCCAGAACAACTCTTCTGTCTCAACCTC 555
Qy 58 AlaIleSerAspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeu 77
Db 556 GCCATCTCCGACTTCTCTGGTGGTCCCTTCGCAATCCCATGTGACGTACCTATGTGCTG 615
Qy 78 Phe---AsnTrpAsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeu 96
Db 616 ACCGGCGCTTGGACCTTCGGCGCGGCTCTGCAAGCTGTGGCTGGTGTAGACTACTTA 675
Qy 97 LeuCysThrAlaSerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerVal 116
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Qy 117 SerAsnAlaValArgTyrArgAlaGlnHisThrGlyIleLeuIleValAlaGlnMet 136
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Qy 137 ValAlaValTrpIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSer 156
Db 796 GCACGTGTGGTGGTGGCTTCTCTGCTATGCGGCTGCATCTCTG-----AGT 846
Qy 157 TrpLys-----AsnSerThrAsnThrGluGluCysGluProGlyPheVal 171
Db 847 TGGAGTACCTGTCTGTGGCAGTTCCATCCCGAGGGCCACTCTATGTGTGAGTTCTTC 906
Qy 172 ThrGluTrpTyrIleLeuAlaIleThrAlaPheLeuGluPheLeuProValSerLeu 191
Db 907 TACACTGGTACTTTCATCAGGCTTCACCCCTCGAGTTCTTCAGCCCTTCTCCTCAGC 966
Qy 192 ValValTyrPheSerValGlnIleTyr----- 200
Db 967 GTTACCTTCTCAACCTCAGCATCTACTGACATCCAGAGCGCACCGCCTTCGGCTT 1026
Qy 200 ----- 200
Db 1027 GATGGGGCGGTGAGGCTGGCCAGAACCCACCAGATGCCAGCCCTCGCCACCTCCA 1086
Qy 201 -----TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHis 215
Db 1087 GTTCCCCCAGCTGCTGGGGCTGTGGCCAAAGGGCATGGCGAGGCCATGCGGTTGCAC 1146
Qy 216 AlaGlyPheIleAlaThrSerSerArgGlyThr-----Gly 227
Db 1147 AGGTATGGGTGGTGGAGCGGCTGTGTGAGCTGGGAGGGCTGCTCGGGGT 1206
Qy 228 HisSerArgArgThrGlyLeuAlaCysArgThrSerLeuProGlyLeuLysGluProAla 247
Db 1207 GGCAGTGGTGGAGTGTGCTGCTCCGCCACCTCCAGCTCTGCG-----AGC 1254
Qy 248 AlaSerLeuHisSerGluSerProArgGlyLysSerSerLeuValSerLeuArgThr 267
Db 1255 TCCTCAAGGGGCACTGAGAGGCCACGC----- 1281
Qy 268 HisMetSerGlySerIleAlaPheLysValGlySerPheCysArgSerGluSerPro 287
Db 1282 -----TCACTCAAAGGGGCTCCAGGCATCAGCATCTTCAGCA 1320
Qy 288 ValLeuHisGlnArg-----GluHisValGluLeuLeu 298
Db 1321 TCCCTGAGAAGCGCATGAGATGGTGTCCAGAGCATCACCCAGCGCTTCGCGCTGTGC 1380
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Db 1441 GCGCGGTACACGGCTCTTAATGATCATCCGAGCTGCTTGC---CATGGCCGCTGCATCCCC 1497
Qy 339 SerIleTrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnProPhe 358
Db 1498 GATTACTGGTACGAGAGCTCTTCTGTGGTGGCCAACTGGCGGTCAACCCGTC 1557
Qy 359 LeuTyrProLeuCysHisArgPheGlnLysAlaPheTrpLysIleLeuCysValThr 378
Db 1558 CTCTACCCACTGTGCCACTACAGCTTCGCGAGAGCCCTTACCAGACTCTCTGCCCCCAG 1617
Qy 379 Lys-----GlnProAlaProSerGlnThrGln 387
Db 1618 AAGCTCAAGGTCCAGCCGCCAGCGCTCCCTGGAGCAG 1653

RESULT 3
US-11-136-527-127
; Sequence 127, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 127
; LENGTH: 2824
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-127

Alignment Scores:
Pred. No.: 3,61e-45 Length: 2824
Score: 621.00 Matches: 151
Percent Similarity: 46.1% Conservativeness: 48
Best Local Similarity: 35.0% Mismatches: 145
Query Match: 30.4% Indels: 88
DB: 14 Gaps: 10

US-10-626-126-9 (1-391) x US-11-136-527-127 (1-2824)
Qy 18 LeuAlaPheLeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAenAlaValValle 37
Db 446 CTGGCTGGCTCATGGCGCTGCTCATGTGGCCACAGTACTGGGCAACGGCTGGTCATG 505
Qy 38 LeuAlaPheValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeu 57
Db 506 CTCGCTTCGTGGCGGATTCGAGGCTCCGACCCAGAACAACTCTTCTGTCTCAACCTC 565
Qy 58 AlaIleSerAspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeu 77
Db 566 RSSAKTCSGACWKSSTGCTGGTGGTGGCTTCTGTGATCCCATGTGACGTACCTATGTCTG 625
Qy 78 Phe---AsnTrpAsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeu 96
Db 626 ACCGGCGCTTGGACCTTCGGCGCGGCTCTGCAAGCTGTGGCTGGTGTAGACTACTTA 685
Qy 97 LeuCysThrAlaSerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerVal 116
Db 686 CTGTGTGCTTCTCGGTCTTCAACATCGTACTCATCAGCTATCAGCATTCCTGTCTGATC 745
Qy 117 SerAsnAlaValArgTyrArgAlaGlnHisThrGlyIleLeuLysIleValAlaGlnMet 136
Db 746 ACTCGAGTGTCTTCTTACAGGGGCCAGCAGGGGGGACACAGACGGGCGCTTCGGAAGATG 805
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Qy 139 ValThrIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLys 158
 Db 574 GTTTGGGTGGCGCTCTTAGTGAATGGGCAATGATTTAGTTTCAGAGTCTTGGAG 633
 Qy 159 AsnSerThrAnthrGluGluCyseGluProGlyPheValThrGluTrpTyrIleLeuAla 178
 Db 634 GATCAAGGTAGT-----GAATGTGAACCTGGATTTTTCGGAAATGGTACATCTTGCC 687
 Qy 179 IleThrAlaPheLeuGluPheLeuProValSerLeuValValTyrPheSerValGln 198
 Db 688 ATCATCATCATCTTCTGGAATTCGTGATCCAGTCATCTTAGTCGTCTATTTCACATGAAT 747
 Qy 199 IleTyrTrpSerLeuTrpLysArgGlySerLeu 209
 Db 748 ATTTATTGGAGCCTGTGGAAGCGTGATCATCTC 780

RESULT 5
 US-11-136-527-3691
 ; Sequence 3691, Application US/11136527
 ; Publication No. US2005028750A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wyeth
 ; APPLICANT: Mounts, William M
 ; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
 ; FILE REFERENCE: 021896-041000 (AM101086)
 ; CURRENT APPLICATION NUMBER: US/11/136,527
 ; CURRENT FILING DATE: 2005-05-25
 ; PRIOR APPLICATION NUMBER: US 60/574,294
 ; PRIOR FILING DATE: 2005-05-26
 ; NUMBER OF SEQ ID NOS: 362830
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 3691
 ; LENGTH: 2348
 ; TYPE: DNA
 ; ORGANISM: Rattus norvegicus
 US-11-136-527-3691

Alignment Scores:
 Pred. No.: 3,92e-26 Length: 2348
 Score: 407.50 Matches: 136
 Percent Similarity: 40.2% Conservativity: 79
 Best Local Similarity: 25.4% Mismatches: 166
 Query Match: 19.9% Indels: 155
 DB: 14 Gaps: 18

US-10-626-126-9 (1-391) x US-11-136-527-3691 (1-2348)

Qy 4 SerAnGlyThrAspValLeuProLeuThrAlaGln-----ValProLeu 18
 Db 282 TCAACAGACACCTCCAGCGACCCCTCTCGGGGGTCACACCATCTGGCAAGTCGTCTTCATT 341
 Qy 19 AlaPheLeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValValIleLeu 38
 Db 342 GCCTTCTTAACCGGCTCTCGGCAATTGGTGACCATCATTTGGCAACATCTTGTTCATTGTG 401
 Qy 39 AlaPheValAlaAspArgAsnLeuArgHisArgSerAnTyrPhePheLeuAsnLeuAla 58
 Db 402 GCCTTTCAAGGTCAACAAACAGCTGAAGACAGTCAACAACTACTTCTCTTAAGCCTGGCC 461
 Qy 59 IleSerAspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPhe 78
 Db 462 TGTGCAGACCTGTATCATCGGGGTCATTTCCATGAACCTGTTCACTACATCATATTATG 521
 Qy 79 Asn---TrpAnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeu 97
 Db 522 AACCGTTGGGCACATGGGGAATTAGCCTGCACTCTGGCTCTCCATTCATGATATGTGCC 581
 Qy 98 CysThrAlaSerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSer 117
 Db 582 AGCAATGCCCTCTGTCATGAATCTGCTGTCATCAGCTTTGACAGGTACTTTTCCACT 641
 Qy 118 AsnAlaValArgTyrArgAlaGlnHisThrGlyIleLeuLysIleValAlaGlnMetVal 137
 Db 117

Db 642 AGCCCACTACCTACCGAGCCAAAAGAACA-----ACAAAACGAGCTGGTGTGATGATT 695
 Qy 138 AlaVal---TrpIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSer 156
 Db 696 GGTGTGGCTTGGGTGTCATCTCTTGTCTATGGGCTCTGCCATCTTTG-----TTC 746
 Qy 157 Trp-----LysAsnSerThrAnThrGluGluCyseGluProGlyPheVal 171
 Db 747 TGGCAATACCTTTAGGGAAGAGAACTGTGCCCCCAGGAGAAATGTTTCATTCAGTTTCTG 806
 Qy 172 ThrGluTrpTyrIleLeuAlaIleThrAlaPheLeuGluPheLeuProValSerLeu 191
 Db 807 AGTGAGGCCCACTACCTTTGGCAGCGCATCGCTGCTTTTATACATCGCTGTCCACCATC 866
 Qy 192 ValValTyrPheSerValGln-----IleTyr 200
 Db 867 ATGAC-TATTTTATCTGGAGGATCTATAAGAAACTGAGAAGCGTACCAAGAGCTGGC 925
 Qy 201 Trp-----SerLeuTrpLysArg---GlySerLeuSerArgCysProSerHisAlaGly 217
 Db 926 TGGCTTACAGGCTCTCTGGGACAGAAGCGGAGGAGGAGAAACTTTGTCCACCCACAGGAG 985
 Qy 218 Phe-----IleAlaThrSerSerArgGlyThr----- 226
 Db 986 TTCTCGAAGCTGTAGCAGCTATGAACCTGCAACAGCAGAGGTGAAACGATCATCCAGGAG 1045
 Qy 227 -----GlyHisSerArgArgThrGlyLeuAlaCysArgThr 238
 Db 1046 GAAGTACGGTCTGCTGTCTCTGTTTCCACCAAGAGCTGGAAGCGGAGTCCGAGCA 1105
 Qy 239 Ser-----LeuPro 241
 Db 1106 GATGGACCAAGACACAGCAGCAGCAGACAGTGTGGAACAAACAGATGCTGCTGCTCCCT 1165
 Qy 242 Gly-----LeuLysGluProAlaAlaSerLeu 250
 Db 1166 GGAATACTCTGCTCTCCGATGAGAGGACATTTGGCTCAGAGACAGGGCCATCTATT 1225
 Qy 251 HisSerGluSerProArg-GlyLysSerSerLeuLeuValSerLeuArgThrHisMetSe 270
 Db 1226 CATTTGCTCAAGCTTCCAGGCCATAGTCTCACTCTCACTTACCAAGCTTACCATCTC 1285
 Qy 270 rGlySerIle----- 273
 Db 1286 AGATAACCTGCAGGTGTCCAACAGGACCTGGGAGCTGTGGATGTGGAGAGAAATGCTCA 1345
 Qy 273 ----- 273
 Db 1346 CAAGCTTCAGGCCCAGAGAGCATGGGTGATGGTGACAACTGTTCAGAGGATTTTACCNA 1405
 Qy 273 ----- 273
 Db 1406 GCTTCCCATCCAGTTAGAGTCTGTGTGGACACAGGCAAGACCTCTGACACCAACTCTC 1465
 Qy 274 -----IleAlaPheLysValGlySer----- 280
 Db 1466 GGCAGACAAGACCAACCGCTACTCTACTCTGCTCTTCAAGGAGGCCACGCTGGGTAAGAG 1525
 Qy 281 -PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgG 300
 Db 1526 GTTTGCTCTCAAGACCAGAGTCAATCAGATCACCAGCGGAAGAGGATGTGCTCATCAGGA 1585
 Qy 300 YrGlyLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPr 320
 Db 1586 GAAGAGGCCGCCAGAGCGCTCAGTGCCATCTTTGTAGCTTTCATCATCATCAGTGAGCC 1645
 Qy 320 oTyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerI 340
 Db 1646 CTACAACATCATGCTGCTGGTG---AACACCTTCGCGACAGCTGCATACCCAAACCTA 1702
 Qy 340 eTyrTyrSerIleAlaPheTrpLeuGlnTrpPheAnSerLeuIleAsnProPheLeu 360
 Db 1703 TTGG---AATCTGGGCTACTGGCTGTGCTATATCAACAGCAGCCGCTGAACCTGTGTGCTA 1759

QY 360 rProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeu-----CysVa 377
 Db 1760 TGCCTGTGCAACAACAATTCAGAACCACTTCAGATGCTCTCTGTGGCCAGTGTGA 1819
 QY 377 lThrLysGlnProAlaProSerGlnThrGlnSerValSerSer 391
 Db 1820 CAAAAGGAGAGGCGCAACAGCAGTACCAAGCAGACAGACAGTCG 1862

RESULT 6

US-11-127-877-17
 ; Sequence 17, Application US/11127877
 ; Publication No. US20050287565A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Merchiers, Pascal G.
 ; APPLICANT: Hoffmann, Marcel
 ; APPLICANT: Spittaels, Koenraad F. F.
 ; APPLICANT: Laenen, Wendy
 ; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
 ; TITLE OF INVENTION: Amyloid-Beta Protein Production
 ; FILE REFERENCE: P27,800-B USA
 ; CURRENT APPLICATION NUMBER: US/11/127,877
 ; CURRENT FILING DATE: 2005-05-12
 ; PRIOR APPLICATION NUMBER: 60/570,352
 ; PRIOR FILING DATE: 2004-05-12
 ; PRIOR APPLICATION NUMBER: 60/603,948
 ; PRIOR FILING DATE: 2004-08-24
 ; NUMBER OF SEQ ID NOS: 590
 ; SOFTWARE: Patent in version 3.3
 ; SEQ ID NO 17
 ; LENGTH: 1773
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-11-127-877-17

Alignment Scores:

Pred. No.: 4,61e-26 Length: 1773
 Score: 405.00 Matches: 141
 Percent Similarity: 41.7% Conservative: 83
 Best Local Similarity: 26.3% Mismatches: 159
 Query Match: 19.8% Indels: 155
 DB: 14 Gaps: 19

US-10-626-126-9 (1-391) x US-11-127-877-17 (1-1773)

QY 2 SerGluSerAsnGlyThrAspValLeuProLeuThrAlaGln-----Val 16
 Db 148 TCCTCTCCAGACGGTACCAACCGATGACCTCTGGGAGGTGCATACCGTCTGGCAAGTGGTC 207
 QY 17 ProLeuAlaPheLeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValVal 36
 Db 208 TTATCGCTTCTTAACGGGCATCTGGCCCTTGGTGACCATCATCGGCAACATCTCGGTGA 267
 QY 37 IleLeuAlaPheValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsn 56
 Db 268 ATTGTGTCATTAAAGGTCAACAGCAGCTCAAGACGGTCAACAACTACTTCTCTTAAGC 327
 QY 57 LeuAlaIleSerAspPhePheValGlyValIleSerIleProLeuTyrIleProHisThr 76
 Db 328 CTGGCCTGTGCCGATCTGATTATCGGGGTCAATTCAATGAATCTGTTTACGACCTATAC 387
 QY 77 LeuPheAsn---TrpAsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyr 95
 Db 388 ATCATGAATCGATGGGCTTAGGAACTTGGCTGTGACCTCTGGCTTGCCTTGCATGACTAC 447
 QY 96 LeuLeuCysThrAlaSerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSer 115
 Db 448 GTAGCCCAACAATGCCTCTGTTATGAATCTTCGTGTCATCAGCTTTCGACATATCTTTCC 507
 QY 116 ValSerAsnAlaValArgTyrArgAlaGlnHisThrGlyIleLeuLysIleValAlaGln 135
 Db 508 ATCAGGAGCGGCTCAGTACGTCAGGCAACGAACA-----ACAAAGAGAGCGCGGTG 561

QY 136 MetValAlaVal---TrpIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSer 154
 Db 562 ATGATCGGCTGGCTTGGGTGCATCTCTTGTCTGGCTCTCCATCCCTCTG----- 615
 QY 155 AspSerTrp-----LysAsnSerThrAsnThrGluGluCysGluProGly 169
 Db 616 ---TTCTGGCAATACCTTGTGTAAGAGAACTGTGCTCCGGGAGAGTGTTCATTTCAG 672
 QY 170 PheValThrGluTrpTyrIleLeuAlaIleThrAlaPheLeuGluPheLeuProVal 189
 Db 673 TTCCTCAGTAGGCCCAACCACTTACTTTTGGCAGACCATCGCTCTTTTATATGCTGTC 732
 QY 190 SerLeuValValTyrPheSerValGln----- 198
 Db 733 ACCATTATGAC-TATTTTATCTGGAGGATCTATAAGGAAACTGAAAAGCGTACCAAGA 791
 QY 199 IleTyrTrp-----SerLeuTrpLysArgGly---SerLeuSerArgCysProSerHis 215
 Db 792 GCTTGTCTGGCTGCAAGCCTCTGGGACAGGAGGAGAGAGAGAACTTTGTTCACCCAC 851
 QY 216 AlaGlyPheIleAlaThrSerSerArgGlyThrGly----- 227
 Db 852 GGCAGTTTCTCGAAGCTGCAGCAGGTACGAACCTTCAACAGCAAGCATGAAACGCTCCAA 911
 QY 228 -----HisSerArgArgThrGlyLeuAlaCys 236
 Db 912 CAGGAGGAAGTATGGCGCTGCCACTTCTGTTTCAACAACAGAGCTGGAAACCCAGCTC 971
 QY 237 ArgThrSer----- 239
 Db 972 CGAGCAGATGGACCAAGACCAGCAGCAGTGCAGTGTGGAAACAACATGATGCTGCTGC 1031
 QY 240 LeuProGly-----LeuLysGluProAlaAla 248
 Db 1032 CTCCTGGAGAACTCCGCTCTCCACGAGGAGGACATGGCTCGAGCAGAGAGCAT 1091
 QY 249 SerLeuHisSerGluSerProArgGlyLys-SerSerLeuLeuValSerLeuArgThrHi 268
 Db 1092 CTACTCCATCGTCTCAAGCTTCGGGTTCAGCAGCACCATCTCACTCCACCAAGTTACC 1151
 QY 268 sMetSerGlySerIle----- 11 274
 Db 1152 CTCATCGGAACAACCTGCGGTGCTGAGGAGGAGCTGGGATGGTGGACTTGGAGAGGAA 1211
 QY 274 eAlaPheLysVal-----GlySerPheCysArgSer-- 284
 Db 1212 AGCCGACAAGCTGCAGGCCCAAGAGCGTGGAGTGGAGGAGGAGGAGGAGGAGGAGGAG 1271
 QY 285 -----GluSerProVal----- 288
 Db 1272 CTCCAAGCTTCCATCCAGCTAGAGTCAGCGTGGACACAGCTAAGACTTCTGACGTCAA 1331
 QY 288 ----- 288
 Db 1332 CTCCTCAGTGGGTAAAGACACGCGCACTCTACCTCTGTCTTCAAGGAAGCCACTCTGGC 1391
 QY 289 -----LeuHisGlnArgGluHisValGluLeu 298
 Db 1392 CAAGAGGTTTGTCTGGAAGACCAAGAGTCAGACTACTAAGCGGAAGAGATGTCCTGGT 1451
 QY 298 uArgGlyArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTr 318
 Db 1452 CAAGGAGAGAAGACGCGCCAGACCTCAGTGGGATCTTGTGCTTTCATCATCTG 1511
 QY 318 palAProTyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLy 338
 Db 1512 GACCCCATCAACATCATGTCTCTGTG---AACACCTTTTGTGACAGCTGCATATCCAA 1568
 QY 338 sSerIleTrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnProPh 358
 Db 1569 AACCTTTTGG---AATCTGGGTACTGTGCTGTCTATCAACAGCAGCCGCTGAACCCGT 1625
 QY 358 eLeuTyrProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeu-Cys---- 376

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Db 1626 GTGCTATGCTCTGTGCAACAAACATTGAGAACACATTTCAAGATGCTGCTGTGCTGCA 1685
Qy 377 --ValThrLysGlnProAlaProSerGlnThrGlnSerValSer 391
Db 1686 GTGTGACAAACAAAGAGCGCAAGCAGCAGTACAGCAGCAGACAGT 1732
RESULT 7
US-11-124-368A-14
; Sequence 14, Application US/11124368A
; Publication No. US20050287559A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: James J. Devlin
; APPLICANT: May Luke
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; FILE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof
; FILE REFERENCE: CL001524
; CURRENT APPLICATION NUMBER: US/11/124,368A
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,845
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/625,936
; PRIOR FILING DATE: 2004-11-09
; NUMBER OF SEQ ID NOS: 21112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 1974
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-124-368A-14
Alignment Scores:
Pred. No.: 5.28e-26 Length: 1974
Score: 405.00 Matches: 141
Percent Similarity: 41.7% Conservative: 83
Best Local Similarity: 26.3% Mismatches: 159
Query Match: 19.8% Indels: 155
DB: 14 Gaps: 19
US-10-626-126-9 (1-391) x US-11-124-368A-14 (1-1974)
Qy 2 SerGluSerAsnGlyThrAspValLeuProLeuThrAlaGln-----Val 16
Db 148 TCCTCTCCAGCGGTACCCAGCATGACCCCTCTGGAGGTGCATACCGCTGCGCAAGTGGTC 207
Qy 17 ProLeuAlaPheLeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaVal 36
Db 208 TTCATCGCTTCTTAACGGGCACTCTGGCCCTGTGTGACCATCATCGGCAACATCTCTGTA 267
Qy 37 IleLeuAlaPheValAlaAspArgAsnLeuArgHisArgSerAsnTyrPheLeuAsn 56
Db 268 ATTGTGTCAATTAAAGGTCAACAGCAGCTGAAGACGGTCAACAACACTACTTCTCTTAAGC 327
Qy 57 LeuAlaIleSerAspPheValGlyValIleSerIleProLeuTyrIleProHisThr 76
Db 328 CTGGCCCTGTCCGATCATGATATATCGGGGTCAATTCATGAATCTGTTTACGACCTATCATC 387
Qy 77 LeuPheAsn---TyrAsnProGlySerGlyIleCysMetPheThrLeuIleThrAspTyr 95
Db 388 ATCATGTAATCGATGGGCTTAGGAAGACTTGGCCCTGTGACCTCTGGCTTGCATGACTAC 447
Qy 96 LeuLeuCysThrAlaSerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSer 115
Db 448 GTAGCCAGCAATGCTCTGTTATGAATCTTCTGTCATCAGCTTTGACAGATCTTTTCC 507
Qy 116 ValSerAsnAlaValArgTyrArgAlaGlnHisThrGlyIleLeuIleValAlaGln 135
Db 508 ATCAGGCGGCGCTCAGTACCGGCAACGACAA-----ACAAAGAGCGCGGTGTG 561
Qy 136 MetValAlaVal---TyrIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSer 154
Db 562 ATGATCGGTCTGGCTTGGGTCAATCTCTCTTTGCTTTTGGGCTCTCTGCCATCTTG----- 615
Qy 155 AspSerTrp-----LysAsnSerThrAsnThrGluGluCysGluProGly 169
Db 616 ---TTCGGCAATACTTTGTGGAAAGAGAACTGTGCTCGGGAGAGTGTCTCATTTAG 672
Qy 170 PheValThrGluTrpTyrIleLeuAlaIleThrAlaPheLeuGluPheLeuProVal 189
Db 673 TTCCTCAGTAGGCCACCATTTACTTTTGGCACGCCATCGCTGCTTTTATATGCTGTC 732
Qy 190 SerLeuValValTyrPheSerValGln----- 198
Db 733 ACCATTATGAC-TATTTTATATCTGGAGCATCTATAAGGAAACTGAAAAAGCGTACCAAGA 791
Qy 199 IleTyrTrp-----SerLeuTrpLysArgGly-----SerLeuSerArgCysProSerHis 215
Db 792 GCTTGTGGCTGCTCAAGCCTCTGGACAGAGGAGGAGAGACAGAAAACTTTGTCCACCCAC 851
Qy 216 AlaGlyPheIleAlaThrSerSerArgGlyThrGly----- 227
Db 852 GGGCAGTTCTCGAAGCTGACAGCTGACAGCTTACGAACCTTCAACAGCAAGCATGAACCGTCCA 911
Qy 228 -----HisSerArgArgThrGlyLeuAlaCys 236
Db 912 CAGGAGGAAGTATGGCGCTGCCACTTCTGTGTTTCAACAACCAAGAGCTGGAACCCAGCTC 971
Qy 237 ArgThrSer----- 239
Db 972 CGAGCAGATGGACCAAGACCAACAGCAGCAGCTGACAGTGGAAACAACATGATGCTGTGC 1031
Qy 240 LeuProGly-----LeuLysGluProAlaAla 248
Db 1032 CTCCTGGAGAACTCCGCTCTCCGACGAGGAGGACATTTGGCTCCGAGAGAGAGCAT 1091
Qy 249 SerLeuHisSerGluSerProArgGlyLys-SerSerLeuValSerLeuArgThrHi 268
Db 1092 CTACTCCATGCTCAAGCTTCGGGTTCACAGCACCCTCTCACTCCACCAAGTTACC 1151
Qy 268 sMetSerGlySerile-----I 274
Db 1152 CTCATCGACACACTGACAGGTGCTGAGGAGGAGCTGGGATGGTGGACTTGGAGAGGAA 1211
Qy 274 eAlaPheLysVal-----GlySerPheCysArgSer-- 284
Db 1212 AGCCGACAAAGCTGACGCCCAGAAAGAGCTGGAGAGTGGAGGAGCATTTTCCAAAAGCTT 1271
Qy 285 -----GluSerProVal----- 288
Db 1272 CTCCAAGCTTCCCATCCAGCTAGAGTCAGCGTGGACACAGCTAAGACTTCTGACGTCAA 1331
Qy 288 ----- 288
Db 1332 CTCCTCAGTGGTAAAGACGACGCGCATCTPACCTCTCTCTCTCAAGGAAGCCACTCTGGC 1391
Qy 289 -----LeuHisGlnArgGluHisValGluLeuLe 298
Db 1392 CAAGAGTTGCTCTGAAGACCAAGAGTTCAGATCATCAAGCGGAAAGAGTGCCTCGGT 1451
Qy 298 uArgGlyArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTr 318
Db 1452 CAAGGAGAGAAGCGGCCAGACCTCAGTGCATCTTCTGCTTGCCTTCATCATCTTG 1511
Qy 318 pAlaProTyrCysLeuPheThrIleValLeuSerThrTyrArgGlyGluArgProLy 338
Db 1512 GACCCCATACATCATGTTCTGTGTG---AACACCTTTTGTGACAGCTGCATACCCAA 1568
Qy 338 sSerIleTrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnProPh 358
Db 1569 AACCTTTTGG---AATCTGGGCTACTGGCTGTGCTACATCAACAGCAGCCGTGAACCCGT 1625
Qy 358 eLeuTyrProLeuCysHisArgPheGlnLysAlaPheTrpLysIleLeu-Cys--- 376
Db 1626 GTCTATGCTCTGTGCAACAAACATTCAGAACCACTTTCAGAGTGTGCTGTGCTGCCA 1685
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; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2030
; LENGTH: 4095
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-2030

Alignment Scores:
Pred. No.: 3.36e-25 Length: 4095
Score: 400.50 Matches: 135
Percent Similarity: 40.0% Conservative: 79
Best Local Similarity: 25.2% Mismatches: 167
Query Match: 19.6% Indels: 155
DB: 14 Gaps: 18

US-10-626-126-9 (1-391) x US-11-136-527-2030 (1-4095)

QY 4 SerAsnGlyThrAspValLeuProLeuThrAlaGln-----ValProLeu 18
DDB 698 TCAACGACACCTCCACGCGACCTCTCGGGGGTGCACACCATCTGGCAAGTSGTTCATT 757
QY 19 AlaPheLeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValAlaIleLeu 38
DDB 758 GCCTTCTTAACYGCGCTCTCGGCATTGGTGACCATCATTTGGCAACATCCTTGTTCATTGTG 817
QY 39 AlaPheValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAla 58
DDB 818 GCCTTCAAGGTCAACCAACAGCTGAAGACAGTCAACCAACTACTTCTCTTAAAGCCTGGCC 877
QY 59 IleSerAspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPhe 78
DDB 878 TGTGCAGACTGATCATCGGGGTCATTTCTTCCATGAACCTGTCTACCTACCTACATCATATG 937
QY 79 Asn---TrpAsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeu 97
DDB 938 AACCGTGGGCACCTGGGGNACTTAGCCTCGACCTCTGGCTCTCCATTGATGATGTGCC 997
QY 98 CysThrAlaSerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSer 117
DDB 998 AGCAATGCTCTGTGCATGAATCTGTGTGTCATCAGCTTTCACAGGTACTTTTCCATCACT 1057
QY 118 AsnAlaValArgTyrArgAlaGlnHisThrGlyIleLeuValIleValAlaGlnMetVal 137
DDB 1058 AGGCCACTACCTACCGAGCCAAAGAACCA-----ACAAACGASSTGGTGTGATGATT 1111
QY 138 AlaVal---TrpIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSer 156
DDB 1112 GGTCTGGCTGGGTGTCATCTCTTGTCTATGCTATGGCTCTCTGCCATCTTG-----TTC 1162
QY 157 Trp-----LysAsnSerThrAsnThrGluGluCysGluProGlyPheVal 171
DDB 1163 TGGCAATACTTGTAGGGAAGAGAACTGTGCCCCAGGAGAAATGTTTCATTTCAGTTTCTG 1222
QY 172 ThrGluTrpTyrIleLeuAlaIleThrAlaPheLeuGluPheLeuProValSerLeu 191
DDB 1223 AGTGAGCCCAACCATCACTTTCGGACGCGCATCGCTGCCCTTTTACATGCTGTCCACATC 1282
QY 192 ValValTyrPheSerValGln-----IleTyr 200
DDB 1283 ATGAC-TATTTTATCTGGAGGATCTATAGGAACCTGAGAACTGAGAGCTACCAAGAGCTGGC 1341
QY 201 Trp-----SerLeuTrpLysArg---GlySerLeuSerArgCysProSerHisAlaGly 217
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RESULT 10

US-11-127-877-5

; Sequence 5, Application US/11127877

; Publication No. US20050287565A1

; GENERAL INFORMATION:

; APPLICANT: Merckhiers, Pascal G.

; APPLICANT: Hoffmann, Marcel

; APPLICANT: Spittaels, Koenraad F. P.

; APPLICANT: Laenen, Wendy

; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting

; TITLE OF INVENTION: Amyloid-Beta Protein Production									
; FILE REFERENCE: P27,800-B USA									
; CURRENT APPLICATION NUMBER: US/11/127,877									
; CURRENT FILING DATE: 2005-05-12									
; PRIOR APPLICATION NUMBER: 60/570,352									
; PRIOR FILING DATE: 2004-05-12									
; PRIOR APPLICATION NUMBER: 60/603,948									
; PRIOR FILING DATE: 2004-08-24									
; NUMBER OF SEQ ID NOS: 590									
; SOFTWARE: PatentIn version 3.3									
; SEQ ID NO 5									
; LENGTH: 2699									
; TYPE: DNA									
; ORGANISM: Homo sapiens									
US-11-127-877-5									
Alignment Scores:									
2.2e-25 Length: 2699									
400.00 Matches: 135									
41.9% Conservative: 80									
26.3% Mismatches: 144									
19.6% Indels: 154									
14 Gaps: 22									
US-10-626-126-9 (1-391) x US-11-127-877-5 (1-2699)									
QY	5	AsnGlyThrAspVal	-----LeuProLeuThrAlaGln-----	-----ValPro	17				
DB	351	AATGGACCCAGTAATACACAGCCTTTGGAAAGCCACAGCGTGTGGGAAGTCATCACC	410						
QY	18	LeuAlaPheLeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValIle	37						
DB	411	ATTGCAGCTGTGACTGCTGGTAAGCTCATCACCATTGTGGGCAATGCTTGGTTCATG	470						
QY	38	LeuAlaPheValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeu	57						
DB	471	ATCTCTTCAAAGTCAACAGCCAGCTCAAGACAGATTAAACAATATTACCTGTCCAGCTTA	530						
QY	58	AlaIleSerAspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeu	77						
DB	531	GCCTGTGCAGATCTCATCATTTGAATCTTCTCCATGAACCTCTACACCACCTACATCCCTC	590						
QY	78	Phe---AsnTyrAsnProGlySerGlyIleCysMetPheTyrLeuIleThrAspTyrLeu	96						
DB	591	ATGGGAGCTGGGCTCTCGGAGTCTGGTGTGACCTTTGGCTTGCACGTGGACTACGTG	650						
QY	97	LeuCysThrAlaSerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerVal	116						
DB	651	GCCAGCAACGCTTCTGTGTATGAACCTTCTGTGATCAGTTTGTACCGTTACTTTTCCATC	710						
QY	117	SerAsnAlaValArgTyrArgAlaGlnHisThr-----GlyIleLeuLysIle	132						
DB	711	ACAAGACCTTGTACATATCGGCCCAAGCGTACTCCGAAAAGGGCTGGCATCATGATTGGC	770						
QY	133	ValAlaGlnMetValAlaValTyrIleLeuAlaPheLeuValAsnGlyProMetIleLeu	152						
DB	771	TTGGCC-----TGGCTGATCTCTTATCTCTCTGGGGCCCAAGCAATCTTC	815						
QY	153	AlaSerAspSerTrp-----LysAsnSerThrAsnThrGluGluCysGlu	167						
DB	816	TGC-----TGGCAGTACTTGTGGGAAGCGGACAGTTCACCTGGATGAGTGCAC	866						
QY	168	ProGlyPheValThrGluTyrTyrIleLeuAlaIleThrAlaPheLeuGluPheLeu	187						
DB	867	ATCCAGTTTCTCTGTGAGCCACCATCATCTTTTGGCACTGCCATTGTGCTCTTCATATC	926						
QY	188	ProValSerLeuValValTyrPheSerValGlnIleTyrTrpSerLeuTyrLysArg---	206						
DB	927	CTGTCTTCTGTATGACCATCTCTACTGTGATCTTACCGGAAACAGAGAGCGAACC	986						
QY	207	-----GlySerLeuSer-----	213						
DB	987	AAGGACCTGGCTGACCTCCAGGGTTCTGTGACTCTGTGACCAAGCTGTGAGAGAGAAAGCCA	1046						

QY	214	SerHisAlaGlyPheIle	-----	215
DB	1047	GCTCATAGGGCTCTGTTGAGATCTCTGCTTGGCGTGTCTCGACCCACCTGGCCACGGG	1106	
QY	220	-----AlaThrSerSerArgGlyThrGly	-----His	228
DB	1107	GAAAGGAACAGGCTCTCTGCTCATCTCCCGCAGGAGCACTCCACCACTGGGAAGCCA	1166	
QY	229	SerArgThrGly	-----LeuAlaCysArgThr	238
DB	1167	TCCCAAGCCACTGGCCCAAGCGCCAATTGGGCCAAAGCTGAGCAGCTCACCACTGTAGC	1266	
QY	239	SerLeuProGlyLeuLysGlu	-----ProAlaAla	248
DB	1227	AGCTACCTTCTCAGAGGATGAGGACAAGCCCGCCACTGACCTGTCTCTCAAGTGGTC	1286	
QY	249	-----SerLeuHisSerGluSerProArgGlyLysSerSer	-----	260
DB	1287	TACAAGAGCTCAGGTAAGAAAAGCCAGGGGAAGAAATTCAGTGTGAAGAGACTGAGAA	1346	
QY	261	-----	-----LeuLeuVal	263
DB	1347	ACTTTTGTGAAGCTGAAATGAAAAAGTGACTATGACACCCCAAACTACCTTCTGTCT	1406	
QY	264	SerLeuArgThrHis	-----MetSerGlySerIleAlaPheLysValGlySerPhe	281
DB	1407	CCAGCAGCTGCTCATGACCCCAAGAGTCAGAAATGTGTGGCTATAGTTCCGATTGGTG	1466	
QY	282	CysArgSerGluSer	-----	286
DB	1467	GTAAAAGCTGACGGGAACCCAGGAGACCAACAATGGCTGTCAAGGTGAAAAATCATGCC	1526	
QY	287	-----ProValLeu	-----His	290
DB	1527	TGCCCCCTCCAGTGGCCCAAGAACCTTCAACGAAAGCGCTCAATCCCAACCCAGCCAT	1586	
QY	291	Gln-----ArgGluHisValGluLeuLeuArgGlyArgLysLeuAlaArgSerLeu	307	
DB	1587	CAATGACCAACGAAAGAGAGTGTCTTAGTCAAGAGAGAAAGCAGCCAGACACTG	1646	
QY	308	AlaValLeuLeuSerAlaPheAlaIleCysTrpAlaProTyrCysLeuPheThrIleVal	327	
DB	1647	AGTGCATCTCTCGGCTTATCATCATGAGACCCCGTATAACATCATGCTCTGTT	1706	
QY	328	LeuSerThrTyrArgArgGlyGluArgProLysSerIleTyrSerIleAlaPheTrp	347	
DB	1707	---TCTACCTTCTGTCAGCAAGTGTCTCCAGTCCACCTGTGGCAC---TTGGGTATTGG	1760	
QY	348	LeuGlnTrpPheAsnSerLeuLeuAsnProPheLeuTyrProLeuCysHisArgArgPhe	367	
DB	1761	TTGTGCTATGTCAATAGCACTGTCAACCCCACTGTCTATGGCTCTGCAACAGAACCTTC	1820	
QY	368	GlnLysAlaPhe	-----TrpLys	373
DB	1821	AGGAAGACCTTAAAGATGCTGCTCTCTGCGCATGGAAA	1859	
RESULT 11				
US-11-036-196-1495				
; Sequence 1495, Application US/11036196				
; Publication No. US20060078900A1				
; GENERAL INFORMATION:				
; APPLICANT: Mendrick, Donna				
; APPLICANT: Porter, Mark				
; APPLICANT: Johnson, Kory				
; APPLICANT: Higgs, Brandon				
; APPLICANT: Castle, Arthur				
; APPLICANT: Elshoff, Michael				
; TITLE OF INVENTION: Molecular Toxicology Modeling				
; FILE REFERENCE: 44921-5089-US				
; CURRENT APPLICATION NUMBER: US/11/036,196				
; CURRENT FILING DATE: 2005-01-18				
; PRIOR APPLICATION NUMBER: US/10/152,319				

RESULT 11
US-11-036-196-1495
; Sequence 1495, Application US/11036196
; Publication No. US20060078900A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Higgs, Brandon
; APPLICANT: Castile, Arthur
; APPLICANT: Elashoff, Michael
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5089-US
; CURRENT APPLICATION NUMBER: US/11/036,196
; CURRENT FILING DATE: 2005-01-18
; PRIOR APPLICATION NUMBER: US/10/152,319

QY	214	SerHisAlaGlyPheIle	-----	-----	219
DB	1047	GCTCATAGGCTCTGTTCAGATCCTCTTGGCGCTGTCTCGACCCACCCCTGGGCCAGCGG	1106		
QY	220	-----AlaThrSerSerArgGlyThrGly-----	His	228	
DB	1107	GAAAGGAACAGCGCCTCTCTGTGTATCTCTCCGAGGAGCAGCTCCACCACTGGGAAGCCA	1166		
QY	229	SerArgArgThrGly-----	LeuAlaCysArgThr	238	
DB	1167	TCCCAAGCCACTGGCCCAAGCGCAATTGGGCCAAAGCTGAGCAGCTCACCACTGTAGC	1226		
QY	239	SerLeuProGlyLeuLysGlu-----	ProAlaAla	248	
DB	1227	AGCTACCTCTCTCAGAGGATGAGGACAAGCCGCCACTGACCTGTCTCCAAGTGGTC	1286		
QY	249	-----SerLeuHisSerGluSerProArgGlyLysSerSer-----	260		
DB	1287	TACAGAGTCAAGGTAAGGAAGCCCAAGGGAAGATTTCAGTCTGAAGAGACTGAGGAA	1346		
QY	261	-----	LeuLeuVal	263	
DB	1347	ACTTTTGTGAAAGCTGAAACTGAAAAAGTACTATGACACCCCAAACTACCTTCTGTCT	1406		
QY	264	SerLeuArgThrHis-----	MetSerGlySerIleAlaPheLysValGlySerPhe	281	
DB	1407	CCAGCAGCTGTCTCATAGACCAAGAGTCAAGATGTGTGCTTAAAGTTCGATTTGGTG	1466		
QY	282	CysArgSerGluSer-----	286		
DB	1467	GTAAGAGCTGACGGGAACAGGAGACCAACAATGGCTGTCAAGAGGTGAAAATCATGCC	1526		
QY	287	-----ProValLeu-----	His	290	
DB	1527	TGCCCCCTTCCAGTGCCCAAGGAACCTTCAACGAAAGGCTCAATCCCACCCAGCCAT	1586		
QY	291	Gln-----	ArgGluHisValGluLeuLeuArgGlyValGlyLysLeuAlaArgSerLeu	307	
DB	1587	CAATGACCAACAGCAAGAGAGTGTCTAGTCAAGAGAGAGAAAGCAGCCAGACACTG	1646		
QY	308	AlaValLeuLeuSerAlaPheAlaIleCysTyrAlaProTyrCysLeuPheThrIleVal	327		
DB	1647	AGTGCCATTTCTCTGGCTTCATCATCATGACCCCGGTATACATCATGTGCTGCTGTT	1706		
QY	328	LeuSerThrTyrArgArgGlyGluArgProLysSerIleTyrTyrSerIleAlaPheTyr	347		
DB	1707	---TCTACCTTCTGTGACAAAGTGTCTCCAGTCACTCCCTGTGGCAC---TTGGGCTATTGG	1760		
QY	348	LeuGlnTyrPheAsnSerLeuIleAsnProPheLeuTyrProLeuCysHisArgArgPhe	367		
DB	1761	TTGTGTATGTCTATAGTACTGTCAACCCCATCTGTATGCCCTCTGCAACAGACCTTC	1820		
QY	368	GlnLysAlaPhe-----	TrpLys	373	
DB	1821	AGGAAGACCTTTAAGATGTCTTCTGTCCGATGAAA	1859		

; PRIOR FILING DATE: 2002-05-22
 ; PRIOR APPLICATION NUMBER: US 60/292,335
 ; PRIOR FILING DATE: 2001-05-22
 ; PRIOR APPLICATION NUMBER: US 60/297,523
 ; PRIOR FILING DATE: 2001-06-13
 ; PRIOR APPLICATION NUMBER: US 60/298,925
 ; PRIOR FILING DATE: 2001-06-19
 ; PRIOR APPLICATION NUMBER: US 60/303,810
 ; PRIOR FILING DATE: 2001-07-10
 ; PRIOR APPLICATION NUMBER: US 60/303,807
 ; PRIOR FILING DATE: 2001-07-10
 ; PRIOR APPLICATION NUMBER: US 60/303,808
 ; PRIOR FILING DATE: 2001-07-10
 ; PRIOR APPLICATION NUMBER: US 60/315,047
 ; PRIOR FILING DATE: 2001-08-28
 ; PRIOR APPLICATION NUMBER: US 60/324,928
 ; PRIOR FILING DATE: 2001-09-27
 ; PRIOR APPLICATION NUMBER: US 60/330,867
 ; PRIOR FILING DATE: 2001-11-01
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 2221
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 1495
 ; LENGTH: 3578
 ; TYPE: DNA
 ; ORGANISM: Rattus norvegicus
 ; FEATURE:
 ; OTHER INFORMATION: Genbank Accession No. NM_012527
 US-11-036-196-1495

 Alignment Scores:
 Pred. No.: 3,48e-25 Length: 3578
 Score: 399.50 Matches: 136
 Percent Similarity: 40.1% Conservative: 80
 Best Local Similarity: 25.3% Mismatches: 162
 Query Match: 19.5% Indels: 161
 DB: 11 Gaps: 18

 US-10-626-126-9 (1-391) x US-11-036-196-1495 (1-3578)

 QY 4 SerAsnGlyThrAspValLeuProLeuThrAlaGln-----ValProLeu 18
 DB 191 TCACACACACCTCCAGGACCCCTCTCGGGGTGACACCATCTGGCAAGTGTTCATT 250

 QY 19 AlaPheLeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValIleLeu 38
 DB 251 GCCTTCTAACTGGCTTCTGCGCATGCTGACCATCATTTGGCAACATCTTGTTCATTGTG 310

 QY 39 AlaPheValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAla 58
 DB 311 GCCTTCAAGGTCAACAAACAGCTGAAGACAGATCAACAACTACTTCTTTAAGCCTGGCC 370

 QY 59 IleSerAspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPhe 78
 DB 371 TGTGCAGACCTGATCATCGGGTCAITTCATGAACCTGTTCACCTACTACATCATATTATG 430

 QY 79 Asn---TrpAsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeu 97
 DB 431 AACCGTGGGCACCTGGGGAACTTAGCTGCGACCTCTGGCTCTCCATTGACTATGTGGCC 490

 QY 98 CysThrAlaSerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSer 117
 DB 491 AGCAATGCCCTGTGCATGAATCTGCTGTCATCAGCTTTGACAGGTACTTTTCACACT 550

 QY 118 AsnAlaValArgTyrArgAlaGlnHisThr-----GlyIleLeuIleVal 133
 DB 551 AGGCCACTCACCTACCGAGCCAAAGAACACAAACAGACGTGTGTGATGATTGGTCTG 610

 QY 134 AlaGlnMetValAlaValTrpIleLeuAlaPheLeuValAsnGlyProMetIleLeuAla 153
 DB 611 GCT-----TGGGTCACTCTCTTGTCTATGGGTCTCTGCCACTCTG--- 652

 QY 154 SerAspSerTrp-----LysAsnSerThrAsnThrGluCysGluPro 168

Db 653 -----TTCTGGCAATACTTTGTAGGAAGAAGAACTGTGCCCCCAGGAGATGTTTCATT 706
 QY 169 GlyPheValThrGluTrpTyrIleLeuAlaIleThrAlaPheLeuGluPheLeuPro 188
 Db 707 CAGTTTCTGAGTGAGCCACCATCACCCTCGGCAGCGCATCGCTGCTTTTACATGCT 766
 QY 189 ValSerLeuValValTyrPheSerValGln----- 198
 Db 767 GTCCACCATCATGAC-TATTTTATCTGGAGGATCTATAAGGAAACTGAGAAGCCTACCAA 825
 QY 199 ---IleTyrTrp-----SerLeuTrpIleArg---GlySerLeuSerArgCysProSer 214
 Db 826 AGAGCTGGCTGGCTACAGSCCTCTGGACAGAAGCGGAGCGACAGAAACTTGTCCACCC 885
 QY 215 HisAlaGlyPhe-----IleAlaThrSerSerArgGlyThr--- 226
 Db 886 CACAGGCAGTTCTCGAAGCTGTAGCAGCTATGAACATGCAACAGCAGCGGTGAACGATC 945
 QY 227 -----GlyHisSerArgArgThrGlyLeuAla 235
 Db 946 ATCCAGGAGGAAGTACGTCGCTGTCTACTTCTGTTTCAACCAAGAGCTGGAAGCCOAG 1005
 QY 236 CysArgThrSer----- 239
 Db 1006 TGGCAGCAGATGGACCAACACACAGCAGCGACAGTGGNAACAACAACAGATGCTGC 1065
 QY 240 ---LeuProGly-----LeuLysGluProAla 247
 Db 1066 TGCTCTCCCTGGAAACCTCTGCTTCTCCGATGAAGAGGACATTTGGCTCAGAGACCGGCG 1125
 QY 248 AlaSerLeuHisSerGluSerProArg-GlyLysSerSerLeuValSerLeuArgTh 267
 Db 1126 CATCTATTCCATTTGCTCCTCAAGCTTCCAGGCCATAGCTCCATCTCAACTCTACCAAGCT 1185
 QY 267 rHisMetSerGlySerIle----- 273
 Db 1186 ACCGTCTCAGATAACCTGCAGGTGTCCAAGAGGACCTGGGACTGTGGATGTGGAGAG 1245
 QY 273 ----- 273
 Db 1246 AATGCTCACAAGCTTCAGSCCCAGAGAGCATGGGTGATGGTGACAACCTGTCAAGAGGA 1305
 QY 273 ----- 273
 Db 1306 TTTCAACAGCTTCCCATCCAGTTAGAGTCTGCGTGTGACACAGCGCAAGACCTCTGACAC 1365
 QY 274 -----IleAlaPheLysValGlySer-- 280
 Db 1366 CAACTCTCGGCAGACAAAGACACCGGCTACTCTACCTCTGTCTTCAAGGAGGCCACGCT 1425
 QY 281 -----PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLe 297
 Db 1426 GGCTAAGAGGTTTGTCTCTCAAGACCAAGAGTCAGATCACCACAGCGGAAGAGGATGTCGCT 1485
 QY 297 uLeuArgGlyArgGlyLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCy 317
 Db 1486 CATCAAGAGAGAAAGCGCCGCGCAGACGCTCAGTGCATCTTGTAGCTTCATCATCAC 1545
 QY 317 sTrpAlaProTyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgPr 337
 Db 1546 GTGGACCCCTTACAACATCATGTGCTGGTG---AACACCTTCTGTGACAGCTGCATACC 1602
 QY 337 oLysSerIleTrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnPr 357
 Db 1603 CAAAACCTATTGG---AATCTGGGTACTGCTGTGCTATATCAACAGCAGCCGGAACCC 1659
 QY 357 oPheLeuTyrProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeu----- 375
 Db 1660 TGTGTGCTATGCTGTGCAACAAACATTCAGAACCCACCTTCAAGACGCTCTCTTGTG 1719
 QY 376 ---CysValThrLysGlnProAlaProSerGlnThrGlnSerValSerSer 391

Db 1720 CCAGTGTGACAAAGGAGGCGGCAACAGCGNATCCAGCAGACAGCAGTCG 1771

RESULT 12

US-11-136-527-3114

; Sequence 3114, Application US/11136527

; Publication No. US20050287570A1

; GENERAL INFORMATION:

; APPLICANT: Wyeth

; APPLICANT: Mounts, William M

; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes

; FILE REFERENCE: 031896-041000 (AM101086)

; CURRENT APPLICATION NUMBER: US/11/136,527

; CURRENT FILING DATE: 2005-05-25

; PRIOR APPLICATION NUMBER: US 60/574,294

; PRIOR FILING DATE: 2005-05-26

; NUMBER OF SEQ ID NOS: 362830

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 3114

; LENGTH: 2633

; TYPE: DNA

; ORGANISM: Rattus norvegicus

US-11-136-527-3114

Alignment Scores:

Pred. No.: 1,11e-24 Length: 2633

Score: 392.00 Matches: 120

Percent Similarity: 46.9% Conservativity: 83

Best Local Similarity: 27.7% Mismatches: 160

Query Match: 19.2% Indels: 71

DB: 14 Gaps: 13

US-10-626-126-9 (1-391) x US-11-136-527-3114 (1-2633)

Qy 5 AsnGlyThrAspValLeuPProLeuThrAlaGlnValProLeuAlaPheLeu----- 21

Db 180 AACATCACTGCTTGGACACGAGAAAGGTCCTGGCAGGTGGCCCTTCATCGGGATCACC 239

Qy 22 MetSerLeuAlaPheAlaAlaThrLeuGlyAsnAlaValValLeuAlaPheVal 41

Db 240 ACAGGCTCTGCTCTAGTACAGTCAGCAGGACCACTACTGCTACTCATCTCTTCAAG 299

Qy 42 AlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaLeuSerAsp 61

Db 300 GTCAACACCGAGCTCAAGACAGTCACCAACTACTTCTGCTGAGCTGGCCTGTGCTGAC 359

Qy 62 PhePheValGlyValLeuSerLeuProLeuTyrPheProHisThrLeuPhe---AsnTyr 80

Db 360 CTCATCATTTGGCACTTCTCCATGAACCTCTATACACGTCATCTGCTCATCGGCCACTGG 419

Qy 81 AsnProGlySerGlyLeuCysMetPheTyrLeuThrAspTyrLeuLeuCysThrAla 100

Db 420 GCTCTGGCACATCGGCTGTGACCTCTGCTGGCTGGCTGGACTATGTGGCCAGCAACGCC 479

Qy 101 SerValTyrSerLeuValLeuLeuSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120

Db 480 TCTGTATGAATCTTCTGCTCATCAGCTTTGACCGTTACTTCTGCTGACCGCCCTG 539

Qy 121 ArgTyrArgAlaGlnHisThrGlyLeuLeuGlyLeuAlaGlnMetValAlaVal--- 139

Db 540 AGCTACCGAGCCAAAGGCGCATCTCC-----CGAAGGGCGAGCTCTGATGATGGCCATGCA 593

Qy 140 TrpLeuLeuAlaPheLeuValValLeuGlyProMet-----IleLeuAlaSerAspSerTyr 157

Db 594 TGCGTGTTCCTTCGTGTTCTG-GGCCCGAGCATCTCTTCTGGCAATACCTAGTTGG 652

Qy 158 -LysAsnSerThrAsnThrGluGluCysGluProGlyPheValThrGluTyrTyrIleLeu 177

Db 653 GGAGCGGACAGATCTGGCTGGGAGTGCTACATCCAGTTTCTCTCCCAACCCATCATCAC 712

Qy 177 uAlaIleThrAlaPheLeuLeuPheLeuLeuProValSerLeuValTyrPheSerVa 197

Db 713 TTTTGGCACAGCCATGGCGGCTTCTACCTCCCTGTCAAGGTCATG-----TG 760

Best Local Similarity:	27.4%	Mismatches:	160
Query Match:	18.9%	Indels:	41
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Qy	8	AspValLeuProLeuThrAlaGlnValProLeuAlaPheLeuMetSerLeuLeuAlaPhe	27
Db	599	GACTCCATCGCCCTGCCCTGGAAAGTCTGTGTTGTTGGTAGGCCTCATCACCTTG	658
Qy	28	AlaIleThrIleGlyAsnAlaValIleLeuAlaPheValAlaAspArgAsnLeuArg	47
Db	659	GCCACCAAGCTCTCAAGCCTTTGTATCGTACGGTGTATCGGACCCGGAAGCTGCAC	718
Qy	48	HisArgSerAenTyRPhPheLeuAsnLeuAlaIleSerAepPhePheValGlyValIle	67
Db	719	ACCCGGCTTAACCTACCTGATCGCTCGTGGCAGTCACCTACCTGCTGCTGTCATCCTG	778
Qy	68	SerIleProLeuTyRIleProHisThrLeuPhe--AenTrpAenProGlySerGlyIle	86
Db	779	GTGATGCCCATCAGCACCATGTACACGGTCACTGGACGCTGGACACTAGGCCAGGTGTC	838
Qy	87	CysMetPheTrpLeuIleThrAspTyRLeuLeuCysThrAlaSerValTyRSerIleVal	106
Db	839	TGGACATTCTGGCTGTCTCGTGGATATCACCTGTTCACCTGCTTCCATCATGTCATCTCTG	898
Qy	107	LeuIleSerTyRAspArgTyRGlnSerValSerAsnAlaValArgTyRArgAlaGlnHis	126
Db	899	GTGATGCCCTGGACCGCTACTGGGCCATCACTGATCGGTGGACTATTCTGCTAAAAGA	958
Qy	127	ThrGlyIleLeuIlysIleValAlaGlnMetValAlaValTrpIleLeuAlaPheLeuVal	146
Db	959	ACTCCC---AAAAGGGGGCCCATCATGATCGTGTGTTGGTCTTCTCCATCTCGATT	1015
Qy	147	AsnGlyProMetIleLeuAlaSerAspSerTrpIysAsnSerThrAenThrGluGluCys	166
Db	1016	TCGCTGCCACCCTTCTTC-----TGGCGTCAGCCAAAGCGGAGGAGGAGTG	1063
Qy	167	GluProGlyPheValThrGluTrpTyRIleLeu-----AlaIleThrAlaPheLeuGlu	184
Db	1064	CTGGACTGCTTTGTGAACACCGACCGCTCTCTACAGGTCTACTCCACGGTGGGGCT	1123
Qy	185	PheLeuLeuProValSerLeuValValTyRPhSerValGlnIleTyRTrpSerLeuTrp	204
Db	1124	TTCTATTATCCACCCTGCTCTCATGCGCTCTATGCGCGTATCTATGTGAAGCCCGC	1183
Qy	205	LysArgGlySerLeuSerArgCysProSerHisIalaglyPheIleAlaThrSerSerArg	224
Db	1184	TCCTCGG---ATTTTGAAGACACACCCCAAGACCGGC-----	1219
Qy	225	GlyThrGlyHisSerArgThrGlyLeuAlaCysArgThrSerLeuProGlyLeuLys	244
Db	1220	-----AAGCGTTGACCCGAGCCCGCTGTGATACAGACTCTCCAGGATCCACG	1267
Qy	245	GluProAlaSerLeuHisSerGluSerProArgGlyLysSerSerLeuLeuValSer	264
Db	1368	TCCTCGGTCACTCCATTAACTCCGGGTTCCGGAGGTGCCCACTGAG-----	1315
Qy	265	LeuArgThrHisMetSerGlySerIleIleAlaPheLysValGlySerPheCysArgSer	284
Db	1316	-----TCGGGTCTCTCTGTG-----TACGTGAACCAAGTCMAAGTCGGA	1354
Qy	285	GluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGlyArgGlyLeuAla	304
Db	1355	GTCTCAGACGCCCTGCTGGAAAGAGAAACTCATGCGCGCTAGGGAGCGCAAGCCACC	1414
Qy	305	ArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpIlaProTyRCysLeuPhe	324
Db	1415	AAGACCTAGGGATCAATTTTAGGAGCAATTTATGTTGCTGGCTCCCTCTTTCATCATC	1474
Qy	325	ThrIleValLeuSerThrTyRArgGlyGluArgProIysSerIleTrpTyRSerIle	344
Db	1475	TCCCTGTGTATGCTTATCTGCAAG-----GATGCTGTCTGTTTTCACATG	1519

Qy	345	AlaPhe-----TrrLeuGlnTrpPheAsnSerLeuIleAsnProPheLeu	359
Db	1520	GCATTTTTCAGCTTTTCAATTGGCTATCTTAACTCTCTCATCAACCCCATCATC	1579
Qy	360	TyrProLeuCySHISAGAGPheGlnLYAlaPheTrpLYsIleLeu	375
Db	1580	TACACCATGTCCATGAGGACTTCAACAAGCATTCCTCAAACTGATA	1627
RESULT 14			
US-11-136-527-751			
; Sequence 751, Application US/111336527			
; Publication No. US20050287570A1			
; GENERAL INFORMATION:			
; APPLICANT: Wyeth			
; APPLICANT: Mounts, William M			
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes			
; FILE REFERENCE: 031896-041000 (AM101086)			
; CURRENT APPLICATION NUMBER: US/11/136,527			
; CURRENT FILING DATE: 2005-05-25			
; PRIOR APPLICATION NUMBER: US 60/574,294			
; PRIOR FILING DATE: 2005-05-26			
; NUMBER OF SEQ ID NOS: 362830			
; SOFTWARE: PatentIn version 3.2			
; SEQ ID NO 751			
; LENGTH: 3741			
; TYPE: DNA			
; ORGANISM: Rattus norvegicus			
US-11-136-527-751			
Alignment Scores:			
Pred. No.: 4,25e-23 Length: 3741			
Score: 376.50 Matches: 117			
Percent Similarity: 40.9% Conservative: 81			
Best Local Similarity: 24.2% Mismatches: 165			
Query Match: 18.4% Indels: 122			
DB: 14 Gaps: 15			
US-10-626-126-9 (1-391) x US-11-136-527-751 (1-3741)			
Qy	1	MetSerGluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe	20
Db	1030	ATGTGTGAGGGGAACAGGACA--GCCATGGCCAGCCCTCAGCTGTCTGCCCTGGTGGTG	1086
Qy	21	LeuMetSerLeuLeuAlaPheAlaIleThrIleGly---AsnAlaValValIleLeuAla	39
Db	1087	GTTCYTMAGTAGTATCTCCCTG--GTCACAGTGGGCCCTCAACCTCTGGGTGCTGTATGCW	1143
Qy	40	PheValAlaAspArgAsnLeuAlaArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIle	59
Db	1144	GTGRCAGTGARGCGCAAGCTACACCGTGGGCAACCTRTACATTTGTTCAGCTGTCTGKTR	1203
Qy	60	SerAspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPhe---	78
Db	1204	GCAGACCTGATTTGAGGGGAGTGTATGCCCATGAACATCTCTATCTATCATGCATGAC	1263
Qy	79	AsnTrpAsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCys	98
Db	1364	AAGTGGTCCVTGGGCCGCCCTCTGCTCTTTTGGCTTCTATGGGATTAATGGCCAGC	1323
Qy	99	ThrAlaSerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsn	118
Db	1324	ACRGCATTCATCTTTAGYGTCTTACCTCTGTGTATGATCGCTACCGCTCVGTCCAGCAA	1383
Qy	119	AlaValArgTyrArgAlaGlnHisThrGlyIleLeuIleValAlaGlnMetValala	138
Db	1384	CCCTCCGGTACCTGAGGTAYCGAACCAAG--ACCGKGGCTTCMGCTACCATCTCTGGG	1440
Qy	139	ValTrpIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLys	158
Db	1441	GCCTGGTYYTCTCTTCCTTCCTGGGTATACCATACTT-----GGCTGGCAT	1488
Qy	159	Asn-----SerThrAsnThrGluGluCysGluProGlyPheValThr	172


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Qy 260 SerLeuLeuValSerLeuArgThrHisMetSerGlySerIleIleAlaPheLys---Val 278
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2476 TCCGAGGTGGTT---CTGAGGATCCACGTGTCGGCGCCAGCGACCGCCAAAGGATAT 2532
Qy 279 GlySerPheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeu 298
Db |||:::||| |||:::||| |||:::||| |||:::||| |||:::||| |||:::|||
2533 CCCGGAACACAGAGTAGCAGGGCCACACCTTGGCAGCTCGCTTCCGTGAGGCTGCTC 2592
Qy 299 -----ArgGlyArgGlyLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAla 315
Db |||:::||| |||:::||| |||:::||| |||:::||| |||:::||| |||:::|||
2593 AAGTTTTCCTCCGCGAGAAAAGGCTGCCAAGACGTTGGCCATCGTGGGTGTCTTCGTC 2652
Qy 316 IleCysTrpAlaProTyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGlu 335
Db |||:::||| |||:::||| |||:::||| |||:::||| |||:::||| |||:::|||
2653 CTGTGCTGTTCCCTTC---TTCTTCGTCTGCTCTGGGCTCTCTGTTCCCGAGCTG 2709
Qy 336 ArgProLysSerIleTrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIle 355
Db |||:::||| |||:::||| |||:::||| |||:::||| |||:::||| |||:::|||
2710 AAACGGTCAGAGGGTGTTCTCAAGGTATCTTCTGGCTGGGCTACTTCAATAGTGTGTG 2769
Qy 356 AsnProPheLeuTyrProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeu 375
Db |||:::||| |||:::||| |||:::||| |||:::||| |||:::||| |||:::|||
2770 AACCGGTCACTACCCCTGCTCCAGTCGCGAGTTCAAGCGGCTTCTCCGCTCCTG 2829
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Search completed: April 29, 2006, 03:46:03
Job time : 5410 secs

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